STIC-Biotech/ChemLib

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Fr m:

Bunner, Bridget

Sent:

Thursday, February 06, 2003 11:54 AM STIC-Biotech/ChemLib

To: Subject:

sequence search

Hi! I'd like a sequence search performed for case 09/762,594:

1. the nucleic acid sequence of SEQ ID NO: 2

Thanks!

Bridget Bunner

Art Unit 1647 CM1-10D12 (703) 303-7148 mailbox 10B19

> Point of Contact: Susan Hanley Technical Info. Specialist CM1 6B05 Tel: 305-4053

Searcher:_____Phone:______
Location:______
Date Picked Up:_____
Date Completed:______
Searcher Prep/Review:_____
Clerical:_____
Online time:_____

TYPE OF SEARCH:

NA Sequences:

AA Sequences:

Structures:

Bibliographic:

Litigation:

Full text:

Patent Family:

Other:

VENDOR/COST (where applic.)
STN:____
DIALOG:_
Questel/Orbit:___
DRLink:_
Lexis/Nexis:__
Sequence Sys.:_
WWW/Internet:_
Other (specify):____

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Copyright (c) 1993 - 2003 Compugen Ltd.
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					SUMMARIES	
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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
	1459	100.0	:	:		PBR-associated pro
7	1079.6	74.0	3399	22	AAK52051	Human polynucleoti
m	1073.2					Human NTAP CDNA Cl
4	1045.4			22	AAK53035	Human polynucleoti
S	634.8			21	AAA93116	Human secreted pro
9	293.2			21		Human ORFX ORF2918
c 7	268.2					Murine transport a
œ	222.4					Human ORFX ORF3021
σ	204.4					DNA encoding human

044408844

Human immune/haema DNA encoding human Human brain expres Human brain expres Human brain expres Human bone marrow Probe #1164 used Human genome-deriv Human foetal liver Human bone marrow Probe #25870 used Human bone marrow Probe #25870 used Human genome-deriv Probe #25870 used Human genome-deriv Drosophila melanog Human genome-deriv Drosophila melanog Human prostate exp Human cervical can Polyglutamine trac Human prostate exp	S DNA .	ceptor; PBR; PBR- associated protein; cell death; cytostatic; neuroprotective; cerebroprotective; atherosclerosis; stasses; developmental disorder; stress; neurodegenerative disorder; rs
AAK77371 ABK24345 ABK24345 ABK24345 AAK1364 AAK37154 AAK37154 AAK37149 AAK31145 AAK31149 AAK51149 AAK7507 AAK7507 AAK77507 AAK77507	AAA31290 AAF82901 AAV73487 AAV73487 AAS68546 AAAS68546 AAA223895 AAV55831 AAAA5055831 AAA55831 AAA55831 AAA55831 AAA55831 AAA55831 AAA55831 AAA55831 AAA55831 AAA55831 AAA55831 AAA565831 AAA6275831 AAA64275 AAA64275 AAA64275	ne receptor; PBR; cer; cell death; lity; cerebroprot; eimer's disease; sis; stress; neur; 7; ss. lifiers
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43843 43843 527 527 554 554 306 306 306 306 306 306 306 306 306 495 573 573 684		benzodiazepine rece feration; cancer; ce; antinfertility; cr tumour; Alzheimer's ltiple sclerosis; st; stroke; PAP7; ss. cocation/Qualifiers 8.1399 /*tag= a /product= "PAP7" 99WO-US18507.
9877777777777799888	dard; (first dard; dard)	llife CC; t mulli er;
10. 142.6 11. 129 113.4 113.1 110.6 115. 110.6 1	74.2 74.2 74.2 74.2 74.2 74.2 72.6 72.6 72.6 72.6 72.6 72.6 72.6 72	Peripheral-type benzodiazepine re PAP; cell proliferation; cancer; immunoadulator; antiinfertillty; Niemann-Pick C; tumour; Alzheimer cholesterol; multiple sclerosis; immune disorder; stroke; PAP7; ss Mus sp. Location/Qualifie: CDS (*tag= a /product= "PAP7") w0200009549-A2. 24-FEB-2000. 11-AUG-1999; 99WO-US18507.
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ACGGGAGGAGGAGGAGGCGGCGGATAGAGGAAGAGAGGCTTCGGCTGGAACAGCAAAA

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The invention provides isolated peripheral-type benzodiazepine receptor (PBR) associated proteins (PAPS) and nucleic acids encoding the PAP proteins. The PAP polynuclectides are a source of primers and probes for detection, isolation and amplification. PAP ligands or substrates or antibodies can be labeled and used to detect PAPS, in the diagnosis and prognosis of disease associated with increased cell proliferation, such as cancer, or reduced cell death. The diagnostic methods of the invention can be predictive of diseases involving PBR including allstones, atherosclerosis, Niemann-Pick C, Sitosterolemia, Distrophy, tumor proliferation, Schnyder's corneal crystalline dystrophy, brain disorders including Alzheimer's disease, cholesterol metabolism, cevelopmental abnormalities, demyelinization, Charcot-Marie tooth characteries and such and share and share the propriet of the propriet of the propriet disease, Multiple sclerosis, and share the content of the propriet of the prop
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                                                                                                                                                          Papadopoulos V,
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Sequence 1459 BP; 455 A; 298 C; 403 G; 303 T; 0 other;

; 0 480 180 180 240 240 300 300 360 360 420 480 120 Gaps 9 9 GCTTCTAAATAAGTGTTGTCCTCTCCTCTCGGCATATGTTGCGTCCCACAGAATAGAGAA 1 GAATTCGCGGCCGCGTCGACCTAAAGTTGAGTGTTCACTGTAGTGACCCGTGTGAAGGT AGTITIATITITAAATCAACTITCATIGIGCAAACTAGTAAAAGAIGGCAAAGCCITTCA TCCAACTTATGAAGAAAACTGAAGTTCGTGGCACTGCATAAGCAAGTTCTTTTGGGCCC ATATAACCCAGACACGTCCCCTGAGGTTGGATTCTTTGATGTGTTGGGGGAATGATAGGAG GAATTCGCGGCCGCGTCGACCTAAAGTTGAGTTGTTCACTGTAGTGACCCGTGTGAAGGT GGAAGAAGAAGAAAAAGAAAAGACGGAGGAGGAGCGAAGCCAGCGTGAAGAGAAGA GGAAGAAGAAGAGAAAAGAAAGGCGGAGGAGGAGCGAAGGCAGCGTGAAGAGAAGA **ACGAGAGCGGCTGCAAAAGGAAGAAGAGAGGAGGAAGCGAGAGGAGGAAGACCGGCTGAG** 21; Length 1459; ó Indels .; 0 DB Mismatches 100.0%; Score 1459; 100.0%; Pred. No. 0; 0; Conservative Best Local Similarity Matches 1459; Conserv Query Match 61 61 121 121 181 241 241 301 181 361 361 301 421 421 g ò QQ δ QQ δy g ÓΥ qq δ g δ Dβ δ

BP. 3399

AAK52051 standard; cDNA;

AAK52051 ID AAK

RESULT

CTATCTCCTCAAGTTTGATAATTCCTACTCTCTGTGGAGGTCCAAGTCCGTCTACAG 1380 1381 AGTCTATTATACTAGATAGAGCTGCTGTTCCAAGGTCCGGAGTCCAGGGTTGAGCACAAC 1440 TGAAGAAAAAGCAAAAAAAGAACGCCAACAAGCCTCTGCTGGATGAGATTGTACCTGTGTA CCAGCAGTATCCAGGGAACTACGAACAACAGCAGATTCTCATCCGCCAGCTGCAGGAGCA CCAGCAGTATCCAGGGAACTACGAACAACAGCAGATTCTCATCCGCCAGCTGCAGGAGCA GCACTATCAGCAGTATAAACACCAGGCAGAGCAAACCCAACCTGCACAACAAGAGCAGC ATTACAGAAACAGCAAGAAGTAGTGATGGCTGGGGCCATCATTGCCTGCATCATCAAAGGT GAACACAGCTGGAGCAAGTGGATACACTGTCAGTTAATGGACAGGCCAAAACCCACACTGA AAATTCCGAAAAAGTCCTTGAGCCAGAAGCTGCAGAAGAGCCTTGGAAAATGGACCAAA AGACTCTCTTCCAGTGATTGCAGCTCCATCCATGTGGACAAGACCACAAATCAAAGACTT TAAAGAGAAGATTCGGCAGGATGCAGATTCTGTGATTACAGTACGTCGAGGAGAGTCGT CACCGTCCGAGTCCCGACTCATGAGGAAGGATCATACCTATTTTGGGAATTTGCCACAGA CAGTTATGACATTGGGGTTTGGGGTTTATTTTGAATGGACAGACTCTCCAAATGCTGCTGT TGAAGAAAAAGCAAAAAAGCCCAACAAGCTCTGCTGGTGGATGAGTTGTACCTGTGTA GCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCCAGCAGTATGCAGC 1459 1441 ATGACGTTTAATTTCCTTT ATGACGTTTAATTTCCTTT 841 1021 1021 1081 1081 1141 1141 1201 1201 1261 1261 1321 1321 1441 481 541 601 601 661 721 781 841 901 901 961 961 561 721 781 1381 QQ Ω g Dp qq qq ò QQ Óλ a Op q q Вp g δ pp òγ QQ ò ò ŏ Pp οy δy Qγ g δ ò οy Qγ δ οy

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoded polypeptides (AAM/8023-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammatopolesis requisiting activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                      therapy;
                                                                                                                                                                                                                                                                                                                                                    Υ;
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the sequence listing
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                                                                             vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy .
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ng J, Ren F, Chen
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T, Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Page 2141-2144; 6221pp; English.
                                                                   cell proliferation;
                                            Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                   Drmanac RT,
Wang J, Zhe
Wejhrman T,
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2000us-0560875.
2000us-0598075.
2000us-0620325.
2000us-0654936.
2000us-0663561.
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87.2%;
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                        (first entry)
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Wang D, 1
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                                                                                                                                                                                                                                                                                                                                                                          Yang Y,
                                                                   cytokine;
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                                                                                                                                                  WO200157190-A2
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20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
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                                                                                                                                                                                              05-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammation.
                                                                                                                            Homo sapiens,
                      06-NOV-2001
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AAK52051;
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QA,
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neurotransmission-associated proteins (NTAPS, AAY77121-Y77126). The
present sequence, clone 998868, encodes a benzodiazepine
receptor-associated from a human kidney tumour cDNA library. The NTAPS are
fragments isolated from a human kidney tumour cDNA library. The NTAPS are
used for treatment or prevention of neurological diseases (e.g.,
Alzheimer's, Parkinson's or Huntington's diseases, cerebral neoplasms, or
multiple sclerosis). They can also be used to raise specific antibodies
and to screen for specific binding agents (potential (agonists and
antosociates) NTAP-encoding nucleic acids are useful for recombinant
cantagonists). NTAP-encoding nucleic acids are useful for recombinant
cantagonists, and as a source of therapeutic antagonists
(antisense, triplex-forming or ribozyme molecules). The nucleic acids may
also be used as a source of probes and primers for diagnosis or
cantagoriated or NTAP expression in hybridisation/amplification tests, for
chromosome mapping and for identifying related sequences, and for gene
therapy. NTAP antagonists are used to treat and prevent a wide range of
cancers and immune disorders (e.g. AIDS, asthma, Crohn's disease,
           GCGGTCAAAATCAGTCTACTACAGAGTCTATTATACTAGATAAAAATGTTGTTACAAAGT 1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human neurotransmission associated proteins, useful for treatment, prevention and diagnosis of neurological disease, e.g. Alzheimer's disease, and antagonists for treating cancer or immune disorders \cdot
                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                 Neurotransmission-associated protein; NTAP; benzodiazepine receptor-associated protein; neurological disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; cerebral neoplasm; multiple sclerosis; drug screening; gene therapy; antagonist; cancer; AIDS; asthma; Crohn's disease; osteoporosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GA;
                                                                                                                                                                                                                                                                                                                                                                                       "Human neurotransmission-associated (NTAP) 998868"
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                                                             CCGGAGTCCAGGGTTGAGCACAACATGACGTTTAATTT 1454
                                                                        Corley NC,
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                  BP.
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                                                                                                                                                                                                                           Human NTAP CDNA clone 998868.
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4R, Patterson
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P-PSDB; AAY77123.
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                   detect NTAPs, for diagnosis or monitoring, as therapeutic antagonists, competitive drug screens, and for affinity purification of NTAPs from
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                                                                                                                                                                                                                                                                                                       AGAAAAAGTTGGCAAAGCATTTCATCCAACTTATGAAGAAAAATTGAAGCTTGTGGCACT 129
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                                                                                                                                                             Score 1073.2; DB 21; Length 1481; Pred. No. 1.9e-278;
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                                                                                                               Sequence 1481 BP; 467 A; 289 C; 403 G; 322 T; 0 other;
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osteoporosis, viral or other infections).
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86.9%;
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useful in diagnosis and gene therapy
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vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation; ss.
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Ψ
                                               CCACCAGTATCCAGGGAGGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding polypeptides with cytokine-like activities,
             CCTATTTTGGGAATTTGCCACAGACAGTTATGACATTGGGGTTTGGGGTTTATTTTGAATG
                                        Cao Y,
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Wang Z
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R,
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Chen
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F, C
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Wang J, Zhang J, Ren
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                 Human polynucleotide SEQ ID NO 2564.
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2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
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P-PSDB; AAM79902.
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Wang D,
Yang Y, W
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                                                                                                                                                                                                                                                                                                                             WO200157190-A2
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01-SEP-2000; 2
15-SEP-2000; 2
20-OCT-2000; 2
30-NOV-2000; 2
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20-JUN-2000;
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Zhao QA,
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80322) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                            (AAK52582) and 3666
the sequence listing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | GGATGCCATGGTAGAGTTTGTGAAGCTTCTAAATAAGTGTTGTCCTCTCCTCCTCGGCATA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGAAGGCAGCGTGAAGAAGAACGAGAGGGCGCTGCAAAAGGAAGAAGAAGAAGCGGAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGGCTTCGGTTGGAGCAGCAGAAAGCAGCAGATAATGGCAGCTTTAAACTCCCAGACTGC 814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAACCTGCACAACAACAGGCAGCATTACAGAAACAGCAAGAAGTAGTGATGGCTGGGGC 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGATGTGTTGGGGAATGATAGGAGGAGAATGGGCAGCTCTGGGAAACATGTCCAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGATGCCATGGTGGAGTTTGTCAAGCTCTTAAATAGGTGTTGCCATCTCTTTTCAACATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGGCTTCGGCTGGAACAGCAAAAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.7%; Score 1045.4; DB 22; Length 2350; 86.5%; Pred. No. 7.3e-271;
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from (
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6221pp; English.
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Page 4841-4842;
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Matches 1177; Conserv
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nutritional supplement; immune modulation; autoimmune disorder;
haematopoiesis regulation; tissue growth; haemostasis; inflammation; ss.
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                                                                                                                                                                                                                                              CGAGGAGGAAGAAGAAAACATCGGTTGTGAAGAGAAAGCCAAAAAGAATGCCAACAAGCC
                                                                                                                                                                                          ATACCTATTTGGGAATTTGCCACAGACAGTTATGACATTGGGTTTGGGGTTTATTTGA
                                                                                                                                ATGGACAGACTCTCCAAATGCTGCTGTCAGTGTGCATGTCAGTGAGTCCAGTGACGAGGA
                                                                                                                                                                                                              CAGCCACCAGTATCCAGGGGGGGGGGGTCTATCTCCTCAAGTTTGATAATTCCTACTCTCT
                                                                                                                                                                                                                                       TAATGGACAGGCCAAAACCCACACTGAAAATTCCGAAAAAGTCCTTGAGCCAGAAGCTGC
                          GTGGACAAGACCACAAATCAAAGACTTTAAAGAGAGAATTCGGCAGGATGCAGATTCTGT
                                                                             GGAGGAGGAGGAAGAAATGTCACTTGTGAAGAAAAAGCAAAAAAGAACGCCAACAAGCC
                                                                                                                                                                                    TCTGCTGGATGAGATTGTACCTGTGTACCGGCGGGACTGTCACGAGGAAGTATATGCAGG
                                                                                                                                                                                                                                                                                                                                                     Human secreted protein coding sequence SEQ ID NO: 31
                                                                                                                                                                                                                                                                 GGTCCGGAGTCCAGGGTTGAGCACAACATGACGTTTAATTT 1454
                                                                                                                                                                                                                                                                        AGTCTGGAGTCTAGGGTTGGGCAGAAGATGACATTTAATTT 1695
                                                                                                                                                                                                                                                                                                                                                                                                                             protein"
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/*tag= a
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/product= '98..136
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137..757
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The present sequence is the coding sequence for a human secreted protein. It was isolated from an adult pancreas cDNA library. The proteins and coding sequences of the invention can be used in the isolation of similar genes and proteins, in the elucidation of their function in vivo, and to treat a number of conditions. It is possible that they may have uses as nutritional supplements, as cytokine or cell proliferation factors, in immune modulation, where they may be used to treat immune and autoimmune diseases, as haematopoiesis regulators (treating myeloid or lymphoid cell deficiencies), in the promotion of tissue growth, they may have chemokine or chemotactic activity, haemostatic or thrombolytic activity, or anti-inflammatory activity.
                                                                                                                                                                                                                                                                                                                                                                                           New secreted proteins and polynucleotides encoding them, which are derived from Homo sapiens, useful for therapy, diagnosis, and research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGACCACAAATCAAAGACTTTAAAGAGAAGATTCGGCAGGATGCAGATTCTGTGATTACA 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 CGACCTCAGATCAAAGACTTCAAAGAGAAGATTCAGCAGGATGCAGATTCCGTGATTACA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     641 ATCCGCCAGCTGCAGGAGCAGCACTATCAGCAGTATAAACACCCAGGCAGAGCCAAACCAA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTGCACAACAACAGGCAGCATTACAGAAACAGCAAGAAGTAGTGATGGCTGGGGCCATCA 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITGCCTGCATCATCAAGGTGAACACAGCTGGAGCAAGTGATACACTGTCAGTTAATGGA 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGGCCAAAACCCACACTGAAAATTCCGAAAAAGTCCTTGAGCCAGAAGGTGCAGAAGA 880
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                                                                                                                                                                                                                                                                                                                                                                                                                                        as well as nutritional sources or supplements
                                                                                                                                                                                                                                                                                   Hall J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 40; Page 262-263; 309pp; English
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                                                                                                                                                                                                                                                                                   Hoffman
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                                    99US-0120680.
99US-01298733.
99US-0149639.
99US-0155886.
99US-0157247.
99US-0167823.
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86.2%;
2000WO-US04340
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                                                                                                                                                                                                                                                                                   Yuan O,
                                                                                                                                                                                                                                        (ALPH-) ALPHAGENE INC
                                                                                                                                                                                                                                                                                                                            WPI; 2000-549267/50.
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                                                                                                                                                                                                                                                                                   Valenzuela D,
18-FEB-2000;
                                                                                                                                                                                             15-FEB-2000;
                                                          23-APR-1999;
17-AUG-1999;
                                                                                                                                                  29-NOV-1999;
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                                                                                                                                01-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                    GAGGAAGAAAATGTCACTTGTGAAGAAAAGCAAAAAAGAACGCCCAACAAGCCTCTGCTG 1240
                                                                                                                                                              CAGTATCCAGGGAGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTGTGGAGG 1360
                                                                                                                                                                                                           TCCAAGTCCGTCTACTACAGGTCTATTATACTAGATAGAGCTGCTGTTCCAAGGTCCGG 1420
                      1121 GACTCTCCAAATGCTGCTGTCAGTGTGAGTGAGTCCAGTGACGAGGAGGAGGAG 1180
                                                                                                                 661
                                                                                                                                                                                     721
                                                                                                                                                                                                                                722 TCAAAATCAGTCTACTACAGAGTCTATTATACTAGATAAAAATGTTGTTACAAAGTCTGG 781
422 TTTTGGGAATTTGCCACAGACAATTATGACATTGGGTTTTGGGGTGTATTTTGAATGGACA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and peptides derived from open reading frame X,
                                                                                 CAATATCCAGGGAGGAGTCTATCTCCTCAAGTTTGACAACTCCTACTCTTTGTGGCGG
                                                                                                                                                                                                                        Human ORFX ORF2918 polynucleotide sequence SEQ ID NO:5835.
                                                                                                                                                                                                                                                         AGTCCAGGGTTGAGCACAACATGACGTTTAATTT 1454
                                                                                                                                                                                                                                                                              AGTCTAGGGTTGGGCAGAAGATGACATTTAATTT 815
                                                                                                                                                                                                                                                                                                                                       AAC77363 standard; cDNA; 420 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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antipsoriatic, antiparkinsonian, nootropic; neuroprotective; osteopathic; antiporulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatchic; capulant; vasotropic; antidiabetic; antidiabetic; hypotensive; dermatchic; antidiamentory; antibacterial; antiviral; antifungal; antirheumatic; antidializand and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus capterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, concurred antidicipal antidificanaetory disease; to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine transport and binding associated protein encoding cDNA SEQ ID 327.
                                                                                                                                                                                                                                                 which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                          to AAB43397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGGTTCGTGGCACT 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine; liver; gene library; amino acid synthesis; binding protein; cell metabolism; energy metabolism; fatty acid metabolism; synthesis; phospholipid metabolism; purine; pyrimidine; nucleoside; nucleotide; replication; transcription; translation; transport protein; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCATAAGCAAGTTCTTTTGGGCCCATATAACCCAGACACGTCCCCTGAGGTTGGATTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCATAAGCAAGTTCTTATGGGCCCATATAATCCAGACACTTGTCCTGAGGTTGGATTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGATGTGTTGGGGAATGATAGGAGGAGAGAATGGGCAGCTCTGGGAAACATGTCCAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 293.2; DB 21; Length 420;
Pred. No. 9.2e-69;
0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGAAGGCAGCGTGAAGAAGGAAGAACGAGAGGCGCCTGCAAAAGGAAGAAGAAA
                                                                                                                                                                                                          to AAC77606 encode the proteins given in AAB40237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coagulation; to inhibit thrombosis; and as a contraceptive
useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 420 BP; 134 A; 69 C; 127 G; 88 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 5005; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.1%;
89.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Matches 316;
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antiviral; antibacterial; antifungal;
                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                Shimkets RA,
                                                                                                                                                                                                    31-MAR-1999;
02-APR-1999;
                                                                                                                                                                                                                          05-APR-1999;
                                                                                                                                                        05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                       This invention describes a novel gene library (A) comprises a gene sequence (or its part) encoding a protein involved in amino acid synthesis, cellular/energy metabolism, metabolism of fatty acids/phospholipids, synthesis or breakdown of purines/pyrimidines/nucleosides/nucleotides, DNA replication/transcription/translation, or is a transport/binding protein. (A) are produced that correspond to the 3'-end of mRNA but without the polyA tail. They can be prepared more efficiently and with less effort than conventional libraries. AAK53436-AAK54275 represent fragments of the gene library described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; antisonidasnt; osteopathic; antiarthritic; immunosupressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory;
                                                                                                                                                       Gene library containing sequences with specific 3'-ends and no polyA tail, encoding proteins involved in a wide range of cellular processes
                                                                                                                                                                                                                                                                                                                                                                                                                  1187 GAAAATGTCACTTGTGAAGAAAAAGCAAAAAGAACGCCAACAAGCCTCTGCTGGATGAG 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGGGAGGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTCTGTGGAGGTCCAAG 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCGTCTACTACAGAGTCTATTATACTAGATAGAGCTGCTGTTCCAAGGTCCGGAGTCCA 1426
                                                                                                                                                                                                                                                                                                                                                                                                                              277 GAAAATGTCACTTGTGAAGAAAAAGCAAAAAAGAACGCCAACAACAACGTCTGTGCTGGATGAG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGGGAGGGGAGTCTATCTCTCTCAAGTTTGATAATTCCTACTCTGTGTGGAGGTCCAAG
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0
                                                                                                                                                                                                                                                                                                                                                                       Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ORFX ORF3021 polynucleotide sequence SEQ ID NO:6041.
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                                                                                                                                                                                                                                                                                                                                                                       DB 22;
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                                                                                                                                                                                                                                                                                                                                                 Sequence 278 BP; 69 A; 72 C; 58 G; 79 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 4e-62;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGTTGAGCACATGACGTTTAATTTCCTTT 1459
                                                                                                                                                                                                                                                                                                                                                                       18.4%; Score 268.2; 98.9%; Pred. No. 4e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 15; Page 109; 251pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC77466 standard; cDNA; 291
                                                               2001DE-2003510
                                                                                       99DE-1058160
                                                                                                            (LION-) LION BIOSCIENCE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 98.9
nes 270; Conservative
                                                                                                                                  WPI; 2001-368570/39
                    DE20103510-U1
                                                                 28-FEB-2001;
 Mus musculus.
                                                                                       02-DEC-1999;
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                                           07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC77466;
                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                             Matches
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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary: antipsoriatic; antiportiant; antiarthritic; immunosuppressant; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotrensive; dermatological; immunosuppressive; antidiabetic; hypotrensive; dermatological; antithungal; antirheumatic; antithroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating candidathological conditions associated with an ORFX associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, concurrant has emoglopinaria, antinflammatory disease; to enhance
                                   antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGTGAAGAGGAAGGAGGGGGCTGCAAAAGGAAGAAGAAGAGGGGAAGCGGAGAGGGAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAAGACCGGCTGAGACGGGAGGAGGAGGAGGCGGCGGCGATAGAGGAAGAGAGGCTTCG
antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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Pred. No. 8.8e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for treating e.g. cancers, proliferative disordeneurodegenerative disorders and cardiovascular disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 5226; 5507pp; English.
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0
                                                                                                                                                                                                                                                                                                                                              thrombosis; contraceptive; ss
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99US-0127636.
99US-0127728.
2000US-0540763.
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87.1%;
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21-DEC-1999;
14-MAR-2000;
                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                            21-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                Schlegel R,
                                                                                                                                            19-SEP-2001
                                                                                                                                                                                                                                        14-JUN-2001
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                                                                                                                         AAH72906;
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                                      1397
                                                        242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel human lung cancer polynucleotide (I) and polypeptides (II). (I) and (II) are useful in pharmaceutical compositions, such as vaccines, for the diagnosis and treatment of lung cancer. The polynucleotides are also useful as probes or primers for nucleic acid hybridisation. ABK24314-ABK24397 represent human lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1218 AGAACGCCAACAAGCCTCTGCTGGATGAGATTGTACCTGTGTACCGGGGGGGACTGTCACG 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGAAGTATATGCAGGCAGCCACCAGTATCC-AGGGAGGGGGGGGTCTATCTCCTCAAGTTT 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTCCAGTGACGAGGAGGAGGAGGAAGAAAATGTCACTTGTGAAGAAAAAAGCAAAAA 1217
                             645
3 AGGCCAGCGATGACGACGAGGAGGAAGAAGGAAACATCGGTTGTGAAGAGAAAAGCCAAAA 62
                            CCAGCAGTATGCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGATTCTCATCCG
                                                                                                                                                                                                                                                                                                                                                                                           New lung tumour polypeptides and polynucleotides, useful in
pharmaceutical compositions, such as vaccines, for treating or
preventing lung cancer, or as probes or primers for nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 24; Length 934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Indels
                                                                                                                                                                                                                                                                                                                                                        Switzer
                                                                                                                                                                                          33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 934 BP; 272 A; 176 C; 206 G; 274 T; 6 other;
                                                                                                                                                                                          DNA encoding human lung cancer protein, Seg ID No
                                                                                                                                                                                                           Human; lung cancer; cytostatic; vaccine; gene; ss.
                                                                CCAGCTGCAGGAGCACCACTATCAGCAGTATAAACACCAG 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 204.4; DB 2
Pred. No. 1.1e-44;
                                                                           243 CCAGTTGCAGGAGCAACATTCAGCAGTACATGCAGCAG
                                                                                                                                                                                                                                                                                                                                                       Klee JI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                       Bangur CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 138; 179pp; English.
                                                                                                                                  BP.
                                                                                                                                 ABK24346 standard; cDNA; 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.0%;
84.2%;
                                                                                                                                                                                                                                                                                                       26-MAY-2000; 2000US-207485P.
06-SEP-2000; 2000US-230475P.
                                                                                                                                                                                                                                                                                      2001WO-US17066
                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                        Wang
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-122068/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                               WO200192525-A2
                                                                                                                                                                                                                                                                                                                                                      Harlocker SL,
                                                                                                                                                                                                                                                                                                                                                                                                                        hybridisation
                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                     25-MAY-2001;
                                                                                                                                                                     09-APR-2002
                                                                                                                                                                                                                                                                   06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251;
                                                                                                                                                    ABK24346;
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                           586
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                                                                                                               RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
1337 GATAATTCCTACTCTCTGTGGAGGTCCAAGTCCGTCTACTACAGAGTCTATTATACTAGA 1396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolated nucleic acid for diagnosing and treating cervical cancer for assessing and detecting compounds for treating the cancer \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGCAGCATTACAGAAACAGCAAGAAGTAGTGATGGCTGGGGCATCATTGCCTGCATCAT 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                     TAGAGCTGCTGTTCCAAGGTCCGGAGTCCAGGGTTGAGCACAACATGACGTTTAATTT 1454
                                                                                                                                  CAAAAGGTGAACACAGCTGGAGCAAGTGATACACTGTCAGTTAATGGACAGGCCAAAAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACACTGAAAATTCCGAAAAAGTCCTTGAGCCAGAAGCTGCAGAAGAAGCCTTGGAAAATG
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Pred. No. 4.5e-28;
0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 873 BP; 239 A; 196 C; 196 G; 224 T; 18 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cervical cancer marker nucleic acid 4180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 914-915; 1051pp; English.
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99US-0171350.
200UUS-0189315.
200UUS-0203791.
2000US-0220114.
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                                                                                                                                                                                                                                                                                   AAH72906 standard;
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2000US-0232081
2000US-0232398
2000US-0232399
2000US-0232399
2000US-0232400
2000US-0233063
2000US-0233063
2000US-0233063
2000US-0234223
2000US-0234223
2000US-023423
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2000US-0237040.
2000US-0239935.
2000US-0239937.
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2000US-0241221.
2000US-0241785.
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2000US-0246527
2000US-0246528
2000US-0246612
2000US-0246610
2000US-0246611
2000US-0246611
2000US-0246611
2000US-0246611
2000US-0246611
2000US-0246611
2000US-0246611
2000US-0246611
2000US-0249208
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2000US-0249211.
2000US-0249212.
2000US-0249213.
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2000US-0236368.
2000US-0236369.
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2000US-0244617.
2000US-0246474.
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2000US-0246476.
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2000US-0246524.
2000US-0246525.
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2000US-0249218.
2000US-0249244.
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2000US-0241808.
2000US-0241809.
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2000US-0249264
                    08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
21-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
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-NOV-2000;
-NOV-2000;
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OCT-2000;
OCT-2000;
L-NOV-2000;
S-NOV-2000;
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27-SEP-2000;
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08-NOV-2000;
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08-NOV-2000;
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17-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                         Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                  Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32183
                                                                                                                                                                          AAK77371 standard; DNA; 4384 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0190076.
2000US-0198123.
2000US-0205515.
2000US-0209467.
2000US-021886.
2000US-021886.
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2000US-0217487.
2000US-0217496.
2000US-0218290.
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2000US-0189874
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2000US-0225213.
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2000US-0231243
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                                                                                                                                                                                                                                                                                (first entry)
                            894 GACCAAAAG 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157182-A2
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24 - FEB - 2000;

27 - FEB - 2000;

28 - MAR - 2000;

11 - MAR - 2000;

18 - MAR - 2000;

19 - JUN - 2000;

20 - JUN - 2000;

20 - JUL - 2000;

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26 - JUL - 2000;

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21 - JUL - 2
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14-A0G-2000;
22-A0G-2000;
22-A0G-2000;
22-A0G-2000;
30-A0G-2000;
30-A0G-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
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06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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14-AUG-2000;
                                                                                                                                                                                                                                                                                07-NOV-2001
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                                                                                                                                                                                                                              AAK77371;
                                                                                                                             RESULT 11
                                                                                                                                                AAKY 7371/2

LID AAKY 7371/2

XXX AAX AAKY 7371/2

XXX AAX AAKY 7371/2

DDE Huma Cyto O7-0

WW WW Huma Cyto O9-A

WW Cyto O9-A

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Seq ID No 32.

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foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel human lung cancer polynucleotide (I) and polypeptides (II). (I) and (II) are useful in pharmaceutical compositions, such as vaccines, for the diagnosis and treatment of lung cancer. The polynucleotides are also useful as probes or primers for nucleic acid hybridisation. ABK24314-ABK24397 represent human lung cancer coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1305 ATCCAGGGAGGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTGTGGAGGTCCA 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTCCGTCTACTACAGAGTCTATTATACTAGATAGAGCTGCTGTTCCAAGGTCCGGAGTC 1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AATCAGTCTACTACAGAGTCTATTATACTAGATAAAAATGTNGGTACAAAGTCTGGAGTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATCCAGGGAGAGGAGTCTATCTCCTCAAGNTTGACAACTCCTACTCTTTGTGGCGGNCAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New lung tumour polypeptides and polynucleotides, useful in
pharmaceutical compositions, such as vaccines, for treating or
preventing lung cancer, or as probes or primers for nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 113.4; DB 24; Length 527;
Pred. No. 2.6e-20;
0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human foetal liver single exon nucleic acid probe #11260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 527 BP; 141 A; 103 C; 112 G; 160 T; 11 other;
                                                                                      Human; lung cancer; cytostatic; vaccine; gene;
                                                                                                                                                                                                                                                                                                                                                                                                           Bangur CS, Klee JI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1425 CAGGGTTGAGCACAACATGACGTTTAATTT 1454
                                            DNA encoding human lung cancer protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TAGGGTTGGGCAGAAGATGACATTTAATTT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 138; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.8%;
                                                                                                                                                                                                                                                       25-MAY-2001; 2001WO-US17066.
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ID ABA62955 standard; DNA; 554
                                                                                                                                                                                                                                                                                                 26-MAY-2000; 2000US-207485P.
06-SEP-2000; 2000US-230475P.
09-APR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                           Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-122068/16.
                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 126; Conserv
                                                                                                                                                                       WO200192525-A2.
                                                                                                                                                                                                                                                                                                                                                                                                         Harlocker SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hybridisation
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                                                                                                                                Homo sapiens.
                                                                                                                                                                                                               06-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
control of diseases associated with inappropriate (I) expression of the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
considered may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
connects and cancer metastases of haematopoietic-derived cells. AAK64703
connects and encer metastases of haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK84950 and AAM82169
connects and cancer metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4384 AGAAAAAGGCAAAGCATTTCATCCAACTTATGAAGAAAATTGAAGCTTGTGGCACT 4325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 AGTAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGTTCGTGGCACT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCATAAGCAAGTTCTTTTGGGCCCATATAACCCAGACACGTCCCCTGAGGTTGGATTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 32183; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4384;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4384 BP; 1434 A; 933 C; 758 G; 1259 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 129; DB 22;
Pred. No. 4.5e-24;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 TGATGTTGGGGAATGATAGGAGGAGAATG 249
                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM;
                                                                                                   2000US-0250391.
2000US-0251030.
2000US-0251988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.8%;
90.2%;
                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                2000US-0249300.
2000US-0250160.
                                                                                                                                                                                                                                                                                            2000US-0251990.
2000US-0254097.
                                                                                                                                                                                                                                   2000US-0251868
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                                                                                                                                                                                                                                                                             2000US-0251989
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                                       0000US-0249299
                                                                                                                                                                     2000US-0256719
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                                                                                                 01-05C-2000; 2
05-05C-2000; 2
05-05C-2000; 2
06-05C-2000; 2
08-05C-2000; 2
08-05C-2000; 2
08-05C-2000; 2
08-05C-2000; 2
08-05C-2000; 2
08-05C-2000; 2
                                       17-NOV-2000;
17-NOV-2000;
                                                                             01-DEC-2000;
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metastasis

Rosen CA,

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Gaps

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WO200157277-A2.

09-AUG-2001

Homo sapiens

BP.

ABK24345 standard; cDNA; 527

ABK24345

Query Match

Best Local

157

qq ŏ g δŏ

ò

ABK24345;

Switzer A;

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Homo sapiens.
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                                                                                                                                                                                                                   SG,
                                                                                                                                                                                                                                                                              brains
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AAK37154/c
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                                                                                                                                                                                                                                                                            measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       961 TAAAGAGAAGATTCGGCAGGATGCAGATTCTGTGATTACAGTACGTCGAGGAGAAGTCGT 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1021 CACCGTCCGAGTCCCGACTCATGAGGAAGGATCATACCTATTTTGGGAATTTGCCACAGA 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1081 CAGTIAIGACAIIGGGIIIGGGGIITAATITIGAAIGGACAGACICICCCAAAIGCIGCIGI 1140
                                                                                                                                                                                                                                                                                                                        probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGACTCTCCAGTGATTGCAGCTCCATCCATGTGGACAAGACCACAATCAAAGACTT 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               483 AGTCTCCCCACCTCTGATGGCTCCTCCATGCATCTGGACCTTTGCCAAGGTGAAGGAATT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 TGACTATGACATTGGCTTTGGAGTTTATTTTGACTGGACCCCTGTAACTAGCACTGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 CAAAAGCAAGCTGGGCAAAGAAGAACAGCCGTCTGGTGGTGAAGCGTGGTGAGGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 AACTGTGCAGGTCAGTGATTCCAGTGACGATGAGGATGAAGAAGAGGAAGAG 191
                                                                                                                                                                                                                                                                  probe for
                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver - \,
                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 11260; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                          7.6%; Score 110.6; DB 22; Length 61.1%; Pred. No. 1.5e-19; ive 0; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed single exon probe SEQ ID NO: 11355
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 554 BP; 156 A; 149 C; 114 G; 135 T; 0 other;
                                                                                                                                                                                                                                                                  The invention relates to a single exon nucleic acid
                                                                                                                                                         DR;
                                                                                                                                                         Rank
                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                        Hanzel DK, Chen W,
                                              2000US-0207456.
2000US-0608408.
                                                                                                        04-OCT-2000; 2000GB-0024263.
           2001WO-US00669
                                                                     2000US-0632366.
                                                                               2000US-0234687.
                                                                                             2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.6
Best Local Similarity 61.1
Matches 179; Conservative
                                                                                                                                                                             WPI; 2001-483447/52
                                            26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
           30-JAN-2001;
                                                                               21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                              fetal liver.
probe of the
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                                                                                                                                                        Penn SG,
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ID AAK1
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1081 CAGTTATGACATTGGGTTTGGGGTTTATTTGAATGGACAGACTCTCCAAATGCTGCTGT 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAAAGAGAAGATTCGGCAGGATGCAGATTCTGTGATTACAGTACGTCGAGGAGAAGTCGT 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; SEQ ID NO: 11355; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 554;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                       2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                           21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                          2001WO-US00667
                                                                                                                                                                                    2000US-0180312
                                                                                                                                                                                                                                                                                     2000US-0632366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
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les 179; Conserv
WO200157275-A2
                                                                                                                       30-JAN-2001;
                                                                                                                                                                                                                       26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1021 CACCGTCCGAGTCCCGACTCATGAGGATCATACCTATTTTGGGAATTTGCCACAGA 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 554 BP; 156 A; 149 C; 114 G; 135 T; 0 other;
microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analyzing gene expression in human bone marrow
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Job time : 351 secs
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2000us-0207456.
2000us-0608408.
2000us-0632366.
2000us-0234687.
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Matches 179; Conservative
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                                                                                                               WO200157276-A2
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                                                            Homo sapiens.
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Pp. 64
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Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3

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Run on:

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DB 1; Length 7218;
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Patent No. 5670367
ENERAL INFORMATION:
SAPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE FOLSA
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
US-09-651-011A-3
US-08-285-440-10
US-08-285-440-11
US-08-285-440-11
US-08-630-349-11
US-08-630-349-12
US-08-630-349-13
US-08-630-349-14
US-08-630-349-14
US-09-007-005-32
US-09-007-005-32
US-09-007-005-32
US-09-007-005-32
US-09-007-005-3
US-09-244-796-3
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REGISTRATION NUMBER: 30,768
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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ATTORNEY/AGENT INFORMATION:
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US-08-232-463-14
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COUNTRY:
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   Sequence 20, Appl
Sequence 20, Appl
Sequence 2, Appli
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Sequence 1, Appli
Sequence 1, Appli
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Sequence 15, Appli
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Sequence 93, Appl
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Sequence 17, Appl
Sequence 17, Appl
Sequence 3, Appli
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Patent No. 5489700
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(without alignments)
6678.230 Million cell updates/sec
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Sequence 15,
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Sequence 1,
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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                   5.1.3
Compugen Ltd
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US-08-770-379-20
US-08-770-379-20
US-09-230-371A-20
US-09-249-585A-2
US-09-359-081-2
US-09-359-081-2
US-09-359-081-2
US-08-910-647-1
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US-08-910-647-1
US-08-910-647-1
US-08-910-647-1
US-08-911-15
US-08-914-0888-15
US-08-194-0888-15
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US-08-056-200-93
US-08-800-644-93
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US-09-253-691-3
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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                 GenCore
Copyright (c) 1993
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length: 2000000000
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                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immediate Early Protein From Kaposi's
Sarcoma-Associated Herpesvirus, DNA
Encoding Same And Uses Thereof
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/POCKET UNBER: 0575/52268/JPW/MSC/SKS
TELECOMMULCATION:
TELECOMMULCATION:
   Best Local Similarity 2.6%; Pred. No. 5.7e-18;
Matches 9; Conservative 247; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Partrick S.
TITLE OF INVENTION: Immediate Ear
TITLE OF INVENTION: Sarcoma-Assoc
TITLE OF INVENTION: Encoding Samk
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08728323A
Patent No. 5948676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
2.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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CITY: No
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APPLICANT: Kieff, Elliott D.
APPLICANT: Kaff, Elliott D.
APPLICANT: Kaff, Elliott D.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-10001R
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PALENTIN VET: 2.0
SEQ ID NO 1
                                                                                                                                                                                              2056
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                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                  477 TGAGACGGGAGGAGGAGGAGGCGGCGGGATAGAGGAAGAGAGGCTTCGGCTGGAACAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAGCAGCAGATAATGGCAGCTTTAAAACTCGCAGACTGCCGTGCAATTCCAGCAGTATG
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                                                                                  Length 3489;
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                                                                                                                         Indels
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                                                                                Score 74.2; DB 2;
Pred. No. 5.6e-11;
0; Mismatches 228;
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Pred. No. 5.6e-11;
0; Mismatches 228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09298568 Patent No. 6322792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                 1..3489
                                                                                                     Best Local Similarity
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NAME/KEY:
                   ; LOCATION:
US-08-728-323A-1
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                                                                                                                         Matches 236;
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2177 AGGATGAGCAGCAGCAGCAGGATGAGCAGCAGCAGCAGGATGAGCAGCAGCAGCAGGATG 2236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                        2057 AGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGAGGAGCAGCAGGATGAGC
                                                           477 TGAGACGGGAGGAGGAGGAGGCGGCGGATAGAGGAAGAGGCCTTCGGCTGGAACAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/770,379 FILING DATE:
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SYSTEM: PC-DOS/MS-DOS
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Patent No. 5849564
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5234;
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: DNA (genomic)
US-08-770-379-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MEDIUM TYPE: Floppy
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STATE: New York
COUNTRY: U.S.A.
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  Length 32207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND USES THEREOF
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Score 74.2; DB 2;
Pred. No. 1.9e-10;
); Mismatches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 45185-F
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/08757669A Patent No. 6183751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Ame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chang, Yuan
APPLICANT: BOhenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
  5.1%;
50.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212) 278-0400 (212) 391-0525
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                                          Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
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; GENERAL INFORMATION:
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STATE: New York
                       Similarity
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US-08-757-669A-20/c
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                                       Matches 236;
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SEQ ID NO 2
LENGTH: 1926
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Matches 236;
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US-09-230-371A-20/C

Sequence 20, Application US/09230371A

Patent No. 6348586

GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Russo, James J
APPLICANT: Russo, James J
APPLICANT: Russo, James J
APPLICANT: Moore, Patrick S
APPLICANT: Moore, Patrick S
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES
TITLE OF INVENTION: UNIQUE ASSOCIATED
TITLE OF INVENTION: UNIQUE ASSOCIATED
FILE REFERENCE: 45165-G-PCT-US
CURRENT FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: PCT/US97/13346
PRIOR FILING DATE: 1997-07-22
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENTH: 32207
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                                                                                                                                                        Length 32207;
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                                                                                                                                                                                     0; Mismatches 228; Indels
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5.1%; Score 74.2; DB 4;
Best Local Similarity 50.3%; Pred. No. 1.9e-10;
Matches 236; Conservative 0; Mismatches 228;
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                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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            SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
INFORMATION FOR SEQ ID NO:
                                                                                                                    US-08-757-669A-20
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                                                 AAAAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCCAGCAGTATG 596
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APPLICANT: HOTLICK, ROBERT
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REPERENCE: 0867/00905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DAPE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGAACGAGAGCGGCTGCAAAAGGAAGAAGAAGAAGCGGAAGGAGGAGGAAGACCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     772 ATCAAAGGTGAACACCTGGAGCAAGTGATACACTGTCAGTTAATGGA
Mismatches 228;
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... LOCATION: (1)..(1926)
: OTHER INFORMATION: coding strand of EBNA-1 DNA
US-09-249-5858-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/09249585A; Patent No. 6417002
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Conservative
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536 CAAAAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCCAGCAGTAT
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                                                                                                                                                                   GAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGCAAACCCAACCTGCACAACAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IITLE OF INVENTION: Mammalian Protein Interaction Cloning
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IP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BM PC COMPATIBLE
SOFTWARE: PATENTIAN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,081
FILING DATE: 22-Jul-1999
CLASSIFCATION: CURNOWN>
PRIOR APPLICATION DATA:
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48.9%; Pred. No. 1.3e-10;
7ative 0; Mismatches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
                                                                                                                                                                                                                                                                                                                                           1252 GAGGGCAGGAGGGCAGGAGCAGGAGGGCCAGGAGGGG 1290
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; SEQUENCE DESCRIPTION: SEQ 1D NO: 2:
US-09-359-081-2
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FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/09359081; Patent No. 6316223; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: unknown
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Payan, Don
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Matches 195; Conserv
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                                                                            596 GCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGATTCTCATCCGCCAGCTGCAG
                                                                                                                                                           GAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGCAAACCCCAACCTGCACAACAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Lao, Ying
APPLICANT: Payan, Den
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF INVENTION: System
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 204; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE: US/09/050,863 FILING DATE: 30-MAR-1998
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
                                                                                                                                                                                                                                                                                                                                                      %3-09-050-863-2
; Sequence 2, Application US/09050863
; Patent No. 6114111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 30-MAR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: SILVA, RODIN M.
REGISTRATION UNMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 781-1989
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Matches 195; Conservative
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COMPUTER READABLE FORM:
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STRANDEDNESS:
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STREET: 4
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STATE:
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                                   GAAGAACGAGAGGGGTGCAAAAGGAAGAAGAAGCGGAAGCGAAGCGAGAAGACCGG
                                                                                                     CTGAGACGGGAGGAAGAGAGGCGGCGGATAGAGGAAGAGAGGCTTCGGCTGGAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: HOLLICK, Robert A.
APPLICANT: HOLLICK, Robert A.
APPLICANT: HOLLICK, Robert A.
APPLICANT: Damad, Bassam B.
APPLICANT: Object Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/ID903US1
CURRENT APPLICATION UNMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 5452;
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Patent No. 5976807
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536 CAAAAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCCAGCAGTAT 595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,647
                                                                                                                                                                                                                                            APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Polynucleotide Delivery
                                                                                           1553 GAGGGCCAGGAGGGCCAGGAGCAGGGGCCAGGAGGGG 1515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 204;
                                                       716 GCAGCATTACAGAAACAGCAAGAAGTAGTGGTGGCTGGG
                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                                                                                                                                      Sequence 1, Application US/08910647
Patent No. 6251433
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 121
TELECOMMUNICATION: TELECOMMUNICATION: (510) 923-2706
                                                                                                                                                                                                                                                                                                                                                            STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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INFORMATION FOR SEQ ID NO: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                   CITY: Emeryville
STATE: California
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 195;
                                                                                                                                                   RESULT 11
US-08-910-647-1
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080
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TOPOLOGY:
US-07-884-811-15
                                                                                                                                                                                                                                    JS-07-884-811-15
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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                                                                                                                                                                                                                                                                                                                                                       COMPORTED 18.4.

ZIP: 94608-2916

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                              1298 GAGGGCAGGAGGGCAGGAGGGGCAGGAGGGG 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 72.6; DB 4;
Pred. No. 2.8e-10;
0; Mismatches 204;
                                                          716 GCAGCATTACAGAAACAGCAAGAAGTAGTGATGGCTGGG 754
                                                                                                                                                                                                                                TITLE OF INVENTION: Compositions and Method Polynucleotide Delivery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/620,925 FILING DATE: 21-0u1-2000 CLASSIFICATION: <u href="chick">cunknown></a>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 1218.002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/910,647
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear ; MOLECULE TYPE: DNA (genomic) ; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-620-925-1
                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
                                                                                                                                                                                                                                                                                                             STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542
                                                                                                                                                                    Sequence 1, Application US/09620925 Patent No. 6468986 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 9600 base pairs
                                                                                                                                                                                                                     APPLICANT: Zuckermann et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                             CITY: Emeryville
STATE: California
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Best Local Similarity 48.9
Matches 195; Conservative
                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                     US-09-620-925-1
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                                                                                                                                        RESULT 12
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CORRESPONDENCE ADDRESS: ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
                                                                          GAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGCAAACCCAACCTGCACAACAACAG
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596 GCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGATTCTCATCGCCAGCTGCAG
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                                                                                                                                                                                Mismatches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                       716 GCAGCATTACAGAAACAGCAAGAAGTAGTGATGGCTGGG 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: 5.25 inch, 360 Kb floppy disk IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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48.9%; Pred. No. 3e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: patin (Generatech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/884,811
FILING DATE: 19920518
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME:
                                                                                                                                                                                                                                                                                          Sequence 15, Application US/07884811 Patent No. 5316921 GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Dreger, Ginger R
REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
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EDNESS: single
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596 GCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGATTCTCATCCGCCAGCTGCAG 655
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                                                          536 CAAAAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCCAGCAGTAT 595
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,783A
FILING DATE: 13-Jul-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/884811
FILING DATE: 18-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/885971
FILING DATE: 18-MAY-92
ATTORNEY/AGENT INFORMATION:
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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OPERATING SYSTEM: PC-LUCK...
OPERATING SYSTEM: MinPatin (Genentech)
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TELEPHONE: 415/225-5416
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INFORMATION FOR SEQ ID NO: 15:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Marschang, Diane L. REGISTRATION NUMBER: 35,6 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 10596 base pairs TYPE: Nucleic Acid
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US-08-087-783A-15
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/07885971
Patent No. 532887
GENERAL IMPORMATION:
GENERAL IMPORMATION:
APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R. TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR PROFEASE DOMAIN VARIANTS NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     536 CAAAAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCCAGCAGTAT 595
                                                                                                                                                        656 GAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGCAAACCCAACCTGCACAACAACAG 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356 GAGAAGGAAGAAGAAGAAAAAGAAAAAGAAGCGGAGCGAGCGAAGGCAAGCGTGAAGAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            416 GAAGAACGAGAGCGGCTGCAAAAGGAAGAAGAAGAGAGCGGAAGCGAAGAGGAGGAAGACCGG 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 CTGAGACGGGAGGAAGAAGAGGCGGCGGATAGAGGAAGAGAGGCTTCGGCTGGAACAG 535
                                                                           596 GCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGATTCTCATCCGCCAGCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.0%; Score 72.6; DB 1; Length 10596; 48.9%; Pred. No. 3e-10;
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                                                                                                                                                                                                                                                                          2832 GAGGGCCAGGAGGGGCAGGAGCAGGGGCCAGGAGGGG 2870
                                                                                                                                                                                                                                   716 GCAGCATTACAGAAACAGCAAGAAGTAGTGGTGGCTGGG 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/07/885,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: patin (Generated)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885
FILLING DATE: 19920518
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33,055
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TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 195; Conservative
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US-07-885-971-15
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patent No. 5547856

GENERAL INFORMATION:
   APPLICANT: Godowski, Paul J., Lokker, Nathalie A., Mark, Melanie R.
   TITLE OF INVENTION:
   HEPATOCYTE GROWTH FACTOR VARIANTS
   NUMBER OF SEQUENCES: 22
   CORRESPONDENCE ADDRESS:
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                                          2832 GAGGGGCAGGAGGGCAGGAGCAGGAGGGCCAGGAGGGG 2870
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Pred. No. 3e-10;
); Mismatches 204;
716 GCAGCATTACAGAAACAGCAAGAAGTAGTGATGGCTGGG 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
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us-09-762-594-2.rni
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476 CTGAGACGGGAGGAGGAGGAGGCGGCGGATAGAGGAAGAGGAGGCTTCGGCTGGAACAG 535
                                                                                    536 CAAAAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCCAGCAGTAT 595
                                                                                                                              596 GCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGATTCTCATCCGCCAGCTGCAG 655
                                                                                                                                                                          656 GAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGCAAACCCAACCTGCACAACAACAG 715
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Search completed: February 21, 2003, 21:47:36 Job time : 271 secs

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RESULT 1
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1459
1 gaattcgcggccgcgtcgac......catgacgtttaatttccttt 1459
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1: \cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: \cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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4: \cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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7: \cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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13: \cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
14: \cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           442118 seqs, 280819700 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                                                       OM nucleic - nucleic search, using sw model
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length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

NO.	0.1411111 0.14111111 0.14111110 0.1411110 0.1411110 0.1411110 0.1411110 0.1411110 0.1411110 0.1411110 0.1411110 0.1411110 0.1411110 0.1411110 0.1411110 0.1411110 0.1411110 0.1411110 0.141110 0.1411110 0.1411110 0.14110 0.14110 0.141110 0	Match	Match Length DB 4.8 5524 10 7.8 5527 10 7.8 5527 10 7.8 6 1969 10 7.8 6 1969 10 7.8 7.8 7.8 7.8 7.8 7.8 7.8 7.8 7.8 7.8		US-09-866-562-33 US-09-866-562-33 US-09-866-562-32 US-09-864-761-13381 US-10-101-487-74 US-10-101-487-74 US-09-864-761-3972 US-09-771-208-20 US-09-771-208-20 US-09-968-4761-11284 US-09-962-833-225 US-09-962-833-225 US-09-101-487-73 US-10-101-487-73 US-10-101-487-73 US-10-101-487-73	Sequence 33, Appl Sequence 32, Appl Sequence 32, Appl Sequence 30285, A Sequence 74, Appl Sequence 76, Appl Sequence 3972, Appl Sequence 20, Appl Sequence 22, Appl Sequence 22, Appl Sequence 11284, A Sequence 11284, A Sequence 71, Appl Sequence 73, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl
18	61.8 61.8	4 4	475 512	101	US-09-864-761-1361 US-09-864-761-18121	Sequence 1361, Ap
19	61	4 4	475	10	US-09-884-781-18121 US-09-864-761-6203	Sequence 18121, A Sequence 6203, Ap

Sequence 22817, A Sequence 27984, A Sequence 27, Appl Sequence 19707, A Sequence 19707, A Sequence 2707, Appl Sequence 27093, Appl Sequence 19549, A Sequence 19549, A Sequence 19549, A Sequence 2406, Appl Sequence 36, Appl Sequence 21553, A Sequence 215, Appl Seque	Sequence 18684, A
US-09-864-761-22817 US-09-864-761-22817 US-09-864-761-2784 US-09-864-761-2782 US-09-864-761-19707 US-09-864-761-19707 US-09-864-761-19707 US-09-764-853-937 US-09-764-853-937 US-09-764-853-937 US-09-864-761-1949 US-09-864-761-1949 US-09-864-761-1949 US-09-864-761-1949 US-09-864-761-1949 US-09-864-761-1949 US-09-864-761-1949 US-09-864-761-18143 US-09-864-761-1816 US-09-864-761-1853 US-09-864-761-1853 US-09-864-761-1853 US-09-864-761-8851 US-09-864-761-8851 US-09-864-761-8851 US-09-864-761-8851 US-09-864-761-8851 US-09-864-761-8851 US-09-884-761-8851 US-09-884-761-8851 US-09-884-761-8851	US-09-864-761-18684
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ALIGNMENTS

-SD	US-09-866-562-33
	Sequence 33, Application US/09866562
	FACELL NO. 032002003/30A1 GENERAL INFORMATION:
٠.	APPLICANT: Harlocker, Susan L.
٠.	
٠.	
٠.	
٠.	APPLICANT: Switzer, Anne
•-	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
	IIILE OF INVENTION: AND DIAGNOSIS OF LONG CANCER.
٠.	CURRENT APPLICATION NUMBER: US/09/866,562
••	CURRENT FILING DATE: 2001-05-25
••	NUMBER OF SEQ ID NOS: 96
·.	SEQ ID NO 33
٠.	LENGTH: 934
٠.	TYPE: DNA
1	; ORGANISM: Homo sapiens
3	
OΦ	14.08;
4 Σ	Dest Docal Similarity 04.24; Fred. NO. 2.06-40; Matches 251; Conservative 2; Mismatches 43; Indels 2; Gaps
ΟŸ	1158 AGTCCAGTGACGAGGAGGAGGAGGAAGAAATGTCACTTGTGAAAAAAGCAAAAA 1217
QQ	3 AGGCCAGCGATGACGAGGAGGAAGAAGAACATCGCTTGTGAAGAGAAAAA 62
Qy	1218 AGAACGCCAACAACGCTCTGCTGGATGAGATTGTACCTGTGTACCGGCGGGACTGTCACG 1277
qq	63 AGAATGCCAACAAGCCTTTGCTGGATGAGATTGTGCCTGTGT-CCGACGGGACTGTCATG 121
Qγ	1278 AGGAAGTATATGCAGGCAGCCACCAGTATCC-AGGGAGGGGAG
QQ	122 AGGATGTGTATGCTGGCAGCCATCAATATCCAAGGGAGGAGTCTATCTCCTCAAGTTT 181
ĉ	1337 7.34 - 1304 - 1305
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Ω	182 GACAACTCCTACTTTGTGGCGGTCAAAATCAGTCTACTACTAGTCTATTATACTAGA 241

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APPLICANT: Penn, Sharron G.
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LENGTH: 554
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Sequence 13381, Application US/09864761

Sequence 13381, Application US/09864761

Sequence 13381, Application US/09864761

GENERAL INFORMATION:

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REPERENCE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-09-04

PRIOR FILING DATE: 2000-09-04

PRIOR FILING DATE: 2000-09-07

PRIOR FILING DATE: 2000-09-07
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1397 TAGAGCTGCTGTTCCAAGGTCCGGAGTCCAGGGTTGAGCACAACATGACGTTTAATTT 1454
                             Sequence 32, Application US/09866562; Batent No. US20020009758a1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Harlocker, Susan L.
| APPLICANT: Bangur, Chaltanya S.
| APPLICANT: Mang, Tongtong
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER.
| FILE REFERENCE: 210121.502
| CURRENT APPLICATION NUMBER: US/09/866,562
| CURRENT FILING DATE: 2001-05-25
| SEQ ID NO 32
| LENGTH: 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1425 CAGGGTTGAGCACAACATGACGTTTAATTT 1454
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COTHER INFORMATION: n = A,T,C or G
US-09-866-562-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-864-761-13381/c
                                                                                                                   RESULT 2
US-09-866-562-32
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1081 CAGTTATGACATTGGGTTTGGGGTTTATTTTGAATGGACAGACTCTCCAAATGCTGCTGT 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 TGACTATGACATTGGACTTTATATTTTGACTGGACCCCTGTAACTAGCACTGACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.6%; Score 110.6; DB 10; Length 554; 61.1%; Pred. No. 1.2e-20; tive 0; Mismatches 114; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 AACTGTGCAGGTCAGTGGATTCCAGTGACGATGAGGAAGAGGAAGAGG 191
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N: EXPRESSED IN BRAIN, SIGNAL = 1.9

N: EXPRESSED IN PLACENTA, SIGNAL = 1.8

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.6

N: EXPRESSED IN LUVER, SIGNAL = 1.6

N: EXPRESSED IN LUVER, SIGNAL = 2.4

N: EXPRESSED IN HELA, SIGNAL = 1.7

N: EXPRESSED IN HELA, SIGNAL = 1.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00665
PRIOR PELING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00662
PRIOR PELING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-31
PRIOR PILING DATE: 2000-09-31
PRIOR PILING DATE: 2000-09-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 179; Conservative
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ORGANISM: Homo sapiens
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OTHER INFORMATION: MF.
OTHER INFORMATION: ED.
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APPLICANT: PIETZ, GREGORY E.
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: WAGGONER JR., DAVID W.
TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: 071319/03220
CURRENT APPLICATION NUMBER: US/10/101,487
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION UNMBER: 60/277,705
PRIOR APPLICATION UNMBER: 61/277,705
NUMBER OF SEQ ID NOS: 116
                                                                                                                                                                   1084 TTATGACATTGGGTTTTGGGGTTTTTTTTTTGATGGACAGACTCTCCCAAATGCTGCTGTCAG 1143
                                                                       GGAAGAACGAGAGCGGCTGCAAAAGGAAGAAGAGAGAGCGGAAGCGAGGAGGAGGAGACCG 474
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Pred. No. 3e-09;
); Mismatches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 74, Application US/10101487 Patent No. US20020169125A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LEUNG, DAVID W.
APPLICANT: BERGMAN, PHILIP A.
APPLICANT: LOFQUIST, ALAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 48.6
Matches 190; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (2)..(718)
US-10-101-487-74
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SEQ ID NO 74
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LOCATION: (2)
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                                                                  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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N: EXPRESSED IN PLACENTA, SIGNAL = 1.6

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.6

N: EXPRESSED IN LUNG, SIGNAL = 2.4

N: EXPRESSED IN LUNG, SIGNAL = 2.4

N: EXPRESSED IN HELA, SIGNAL = 1.7

N: M: THIT AF022770.2, EVALUE 3.00e-03

N: M: SYSPROT HIT: P49193, EVALUE 1.30e-01

N: EST_HUMAN HIT: A4292776.1, EVALUE 0.00e+00
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Pred. No. 2.1e-20;
0; Mismatches 113; Indels
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/180, 312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-04
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PRIOR DATE: 2001-01-30
PRIOR PRILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234, 687
PRIOR PRILING DATE: 2000-09-21
PRIOR PRILING DATE: 2001-01-30
                                                                                                               FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30 PPLICATION NUMBER: PCT/US01/0067 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
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Rank, David R.
Hanzel, David K.
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OTHER INFORMATION: S.
OTHER INFORMATION: S.
OTHER INFORMATION: SI
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Matches 177; Conserv
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LENGTH: 306
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APPLICANT: BERGMAN, PHILIP A.
APPLICANT: BERGMAN, PHILIP A.
APPLICANT: BERGMAN, PHILIP A.
APPLICANT: DEGULST, ALAN
APPLICANT: TOMPKINS. CHRISTOPHER K.
APPLICANT: TOMPKINS. CHRISTOPHER K.
APPLICANT: WAGGONER JR., DAVID W.
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 077319/0329
CURRENT APPLICATION NUMBER: US/10/101,487
CURRENT APPLICATION NUMBER: 2002-03-20
FRIOR APPLICATION NUMBER: 60/277,705
FRIOR APPLICATION NUMBER: 60/277,705
SPROR APPLICATION NUMBER: 60/277,705
SPROR APPLICATION NUMBER: 2010-03-21
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 76
LENGTH: 720
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415 GGAAGAACGAGAGCGCCTGCAAAAGGAAGAAGAAGAGCGGAAGCGAAGAGAGAAGACCG 474
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US-10-101-487-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.8%; Score 69.4; DB 9; Length 720; Best Local Similarity 48.6%; Pred. No. 3e-09; Matches 190; Conservative 0; Mismatches 201; Indels
                                                           715 GGCAGCATTACAGAAACAGCAAGAAGTAGTG 745
                                                                                                    679 AGAGGAGGAAGAGGAAGAGAGAGAGAG 709
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                                                                                                                                                                                                         Sequence 76, Application US/10101487 Patent No. US20020169125A1
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US-09-864-761-20733
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TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-09-03
PRIOR PAPLICATION NUMBER: US 60/236,359
PRIOR PAPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR APPLICATION NUMBER: PCT/USO1/00665
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N: EXPRESSED IN ADULT LIVER, SIGNAL = 11
N: EXPRESSED IN BAT44, SIGNAL = 11
N: EXPRESSED IN BRAIN, SIGNAL = 11
N: EXPRESSED IN BRAIN, SIGNAL = 14
N: EXPRESSED IN LUNG, SIGNAL = 14
N: EXPRESSED IN PLACENTA, SIGNAL = 9.8
N: EXPRESSED IN PLACENTA, SIGNAL = 9.4
N: EXPRESSED IN HEART, SIGNAL = 9.4
N: EXPRESSED IN HEALTO, SIGNAL = 11
N: EXPRESSED IN FETAL LIVER, SIGNAL = 12
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4.6%; Score 66.8; DB 10;
Best Local Similarity 49.7%; Pred. No. 1.4e-08;
Matches 196; Conservative 0; Mismatches 197;
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PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLLING DATE: 2000-09-21
PRIOR PPLICATION NUMBER: US 60/234,687
PRIOR PPLING DATE: 2000-09-21
PRIOR PPLING DATE: 2000-09-21
PRIOR PPLING DATE: 2000-09-21
PRIOR PLLING DATE: 2000-09-30
PRIOR PLLING DATE: 2000-09-30
PRIOR PLLING DATE: 2000-09-30
PRIOR PLLING DATE: 2000-06-30
PRIOR PPLICATION NUMBER: US 09/774,203
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APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K.
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TYPE: DNA
ORGANISM: Homo sapiens
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COTHER INFORMATION:
US-09-864-761-20733
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SEQ ID NO 20733
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W: EXPRESSED IN HELA, SIGNAL = 13

W: EXPRESSED IN ADULT LIVER, SIGNAL = 15

W: EXPRESSED IN BT474, SIGNAL = 11

W: EXPRESSED IN BT474, SIGNAL = 11

W: EXPRESSED IN LUNG, SIGNAL = 14

W: EXPRESSED IN BONE MARROW, SIGNAL = 9.4

W: EXPRESSED IN HEART, SIGNAL = 9.4

W: EXPRESSED IN HEART, SIGNAL = 9.4

W: EXPRESSED IN HEART, SIGNAL = 9.4

W: EXPRESSED IN HELLO, SIGNAL = 11

N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.
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Pred. No. 2.7e-08;
); Mismatches 197;
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APPLICANT: HORVAT, SIMON
TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
FILLE REPERENCE: 4077-923710US
CURRENT APPLICATION NUMBER: US/09/771,208
PRIOR PAPPLICATION NUMBER: US 08/999,477
PRIOR FILLING DATE: 1997-12-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAGCATTACAGAAACAGCAAGAAGTAGTGG 749
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  PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21 PRIOR APPLICATION NUMBER: US 09/608,408 PRIOR FILING DATE: 2000-06-30 PRIOR PAPLICATION NUMBER: US 09/774,203 PRIOR FILING DATE: 2001-01-29 NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/09771208 Patent No. US20020155564A1
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                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: E OTHER INFORMATION: E
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Best Local Simil
Matches 196; C
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                                                                                             GAAGAACGAGAGGGCTGCAAAAGGAAGAAGAAGAGCGGAAGCGAGGAGGAAGACCGG
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-09-37
PRIOR PLICATION NUMBER: US 60/236,356
PRIOR PLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: HADREL, David K.
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356
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Pred. No. 2.1e-06;
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OTHER INFORMATION: n is unidentified a, c,
NAME/KEY: miso_feature
LOCATION: (317174)...(317193)
OTHER INFORMATION: n is unidentified a, c,
NAME/KEY: miso_feature
LOCATION: (200353)...(280373)
OTHER INFORMATION: n is unidentified a, c,
NAME/KEY: miso_feature
LOCATION: (271829)...(271848)
OTHER INFORMATION: n is unidentified a, c,
OTHER INFORMATION: n is unidentified a, c,
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LOCATION: (183872)..(183891)
OTHER INFORMATION: n is unidentified a,
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OTHER INFORMATION: n is unidentified a, NAME/KEY: misc.feature.
CATION: (13260)..(132700)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (546998)..(547017)
OTHER INFORMATION: n is unidentified
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LOCATION: (494715)..(494814)
OCHER INFORMATION: n is unidentified
NAME/KEY: misc_feature
                                                                                                                             LOCATION: (123459)..(123478)
OTHER INFORMATION: n is unidentified
                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (602466)..(602485)
OTHER INFORMATION: n is unidentified
                                                                                                                                                                                                                                                                                                                   LOCATION: (39086)..(391005)
OTHER INFORMATION: n is unidentified
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature
; OTHER INFORMATION: n is a, c, g, or
US-09-771-208-20
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               PatentIn version 3.0
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Best Local Similarity 58.5
Matches 113; Conservative
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                                                                            ORGANISM: Mus musculus
                                                                                                            NAME/KEY: misc_feature
NUMBER OF SEQ ID NOS:
                              SEQ ID NO 20
LENGTH: 659158
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US-10-001-870-68
                                                             TYPE: DNA
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APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes a
FILE REFERENCE: DEX-0283
CURRENT PAPLICATION NUMBER: US/10/001,870
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,189
PRIOR FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 225, Application US/09962832
Petent No. US20020110821A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign;
TILLE OF INVENTION: Sets
FILLE REFERENCE: 689290-74
CURRENT APPLICATION NUMBER: US/09/962,832
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,077
PRIOR PELING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
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Pred. No. 3.4e-07;
0; Mismatches 91;
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Pred. No. 3.6e-07;
0; Mismatches 202;
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Best Local Similarity 47.73
Matches 184; Conservative
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Matches 118; Conservative
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APPLICANT: LEUNG, DAVID W.
APPLICANT: LEUNG, DAVID W.
APPLICANT: LEUNG, DAVID W.
APPLICANT: LEONGUIST, ALAN
APPLICANT: LOFQUIST, ALAN
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: TOMPKINS, CHRISTOPHER K.
TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
FILE REFERENCE: 077319/0329
CURRENT APPLICATION NUMBER: US/10/101,487
CURRENT FILING DATE: 2002-03-20
PRIOR FILING DATE: 2001-03-21
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                                                                                                                                                            ; OTHER INFORMATION: MAP TO AC003065.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.53
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.66
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.59
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.52
US-09-864-761-11284
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                         SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 11284
LENGTH: 474
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Pred. No. 2.8e-07;
0; Mismatches 205
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NUMBER OF SEQ ID NOS: 49117
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Best Local Similarity 56.2
Matches 117; Conservative
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                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRI
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; LOCATION: (1)..(522)
US-10-101-487-71
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1216 TGGTGCAGCAGGAGGGCAGCTGAAGCATCTGGTGCAGCAGGAGGGGCAGCTGGAGCAGC 1275
                                                                                 1396 AGGTGGGGCAGCAAAGAACCTGGAGCAGGAGAGAACTGGAGCTCCCAGAGCAGC 1455
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                                                  474 GGCTGAGACGGGAGGAGGAGGAGGCGGCGGATAGAGGAAGAGAGCCTTCGGCTGGAAC
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CURRENT FILING DATE: 2001-05-23
PRIOR PPLICATION NUMBER: US 60/180,312
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-06-26
PRIOR PLILNG DATE: 2000-06-08-3
PRIOR PLILNG DATE: 2000-09-04
PRIOR PPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-10-04
PRIOR PLILNG DATE: 2000-10-13
PRIOR PLILNG DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PRIOR PRIORATE: 2000-09-21
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CURRENT APPLICATION NUMBER: US/09/864,761
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APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen, Wensheng
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RESULT 15
US-10-101-487-69
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Sequence 73, Application US/10101487

Patent No. US20020169125a1

GENERAL INFORMATION:

APPLICANT: LEGUNG, DAVID W.

APPLICANT: PIETZ, GREGORY

APPLICANT: TOMPKINS, CHRISTOPHER K.

APPLICANT: TOMPKINS, CHRISTOPHER K.

APPLICANT: TOMPKINS, CHRISTOPHER K.

APPLICANT: TOMPKINS, CHRISTOPHER K.

TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 077319/0329

CURRENT APPLICATION NUMBER: 60/277,705

PRIOR APPLICATION NUMBER: 60/277,705

PRIOR FILING DATE: 2001-03-21

NUMBER OF SEQ ID NOS: 116

SOFTWARR: PATENTIN VOY: 2.1

SEM ON DATE: 2001-03-21

SOFTWARR: PATENTIN VOY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGCAAACCCAACCTGCACAACAACAG 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||||| ||| ||| ||   || ||   || |||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||  
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                       GAAGAACGAGAGCGCCTGCAAAAGGAAGAAGAAGAAGCGGAAGCGGAGAGGAAGACCGG
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2.8e-07;
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Pred. No.
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Best Local Similarity 47.4%;
Matches 185; Conservative (
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APPLICANT: PIETZ, GREGORY E.
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: WAGGONER JR., DAVID W.
TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES TITLE OF INVENTION: THEREOF FILE REPERBOKE: 077319/0329
CURRENT APPLICATION NUMBER: US/10/101,487
CURRENT APPLICATION NUMBER: 60/277,705
PRIOR APPLICATION NUMBER: 60/277,705
PRIOR PILING DATE: 2001-03-21
NUMBER OF SED ID NOS: 116
SOFTWARE: PATCHILIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
GAGCAGCACTATCAGCAGTATAAACACCCAGGCAGAGCAAACCCAACCTGCACAACAACAG 715
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                                                                           GCAGCCCAGCAGTATCCAGGGAACTACGAACAACAACAGCAGATTCTCATCCGCCAGCTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 62; DB 9; Length 554
Pred. No. 2.9e-07;
0; Mismatches 215; Indels
                                                                                                                                                                                                                                                                                     GCAGCATTACAGAAACAGCAAGAAGTAGTG 745
                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of A OTHER INFORMATION: oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 69, Application US/10101487 Patent No. US20020169125A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FACEL NO. CALL GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LEUNG, DAVID W.
APPLICANT: BERGMAN, PHILIP A.
APPLICANT: LOFQUIST, ALAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.2%;
Best Local Similarity 47.0%;
Matches 191; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
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Search completed: February 21, 2003, 23:59:11 Job time : 1928 secs

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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
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Clone distribution: MGC clone distribution information can. Jeound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10372 row: k column: 08
High quality sequence stop: 680.
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AL546667 AL546667
BG254119 602367007
BG776473 602663560
BG705952 602669271
                                                                                                                                                                                                                                                                       (without alignments)
10658.194 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                      gaattegeggeegetegae.........atgaegtttaattteettt 1459
                                                                                                                                                                                                                            February 21, 2003, 21:36:46; Search time 2217 Seconds
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                         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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542.4
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491.2
487.6
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Minimum DB Maximum DB

Database

Searched:

A1506318 vp71h08.x AA148726 2009b01.r B1965035 id35h05.x

C87779 C87779 Mous C85460 C85460 Mous C85479 C85479 Mous

BG067872 H3059B05

EST 21-FEB-2001

þe

Result 80.

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932 bp mRNA linear EST 02-MAY-2002
AGENCOURT_7551342 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6066023
5', mRNA sequence.
                                                                                                                                                                                                                                     9
                                                       /tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sali; cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full:length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                        DB 12;
                                                                                                                                                                                                       40.9%; Score 597.4; DB 12; 96.6%; Pred. No. 5.9e-131; iive 0; Mismatches 6;
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/organism="Mus musculus"
                                          /clone_lib="NIH_MGC_94"
            /db_xref="taxon:10090"
/clone="IMAGE:4502911"
                                                                                                                                                                                                                                    679; Conservative
                                                                                                                                                                                                                      Similarity
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DEFINITION

ACCESSION

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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pGMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies.
                                                                     Euteleostomi;
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM13343 row: d column: 24
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Pred. No. 4.7e-121;
0; Mismatches 134;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6066023"
/clone_lib="NIH_MGC_72"
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High quality sequence stop: 395.
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llarity 82.8%;
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Mammalia; Eutheria;
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/db xref="taxon:9606"
/clone_itb="CsDiO29y106"
/clone_itb="TITINFO66_PL2"
/tissue_type="placenta"
/tissue_type="placenta"
/tissue_type="placenta"
/rissue_type="placenta"
/ri
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Tai,W.B., Gruber,C., Jessee,J. and normalization
Unpublished (2001)
Contact: Genoscope
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BP 191 91006 EVRY cedex - France
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                       CGTGCAATTCCAGCAGTATGCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGAT
                       TCTCATCCGCCAGCTGCAGGAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGCAAAC
                                                                                                                                                                 CCAACCTGCACAACAAGAAGCAGCATTACAGAAACAGCAAGAAGTAGTGATGGCTGGGGC
                                                                                                                                                                                                            CCAGCTTTCACGGCAACAGGCAGCATTACCGAAACAACCGGAAGTAGTAGTGGCTGGGTC
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Pred. No. 6.4e-118;
1; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAGAAGAAGCCTTGGAAAATGGACCAAAA 901
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BG254119 1108 bp mRNA linear EST 13-FEB-2001 602367007F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4475329 5',
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10300 row. n column: 02
High quality sequence stop: 640.
Location/Qualifiers
                                                                                                        TGATGTGTTGGGGAATGATAGGAGGAGAAATGGGCAGCTCTGGGAAACATGTCCAAGGA
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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/issue_type="mucoepidermoid carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Sil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA.
and 3' adaptors were used in cloning as follows: 5'
adaptors were used in cloning as follows: 5'
adaptors sequence: 5'-ATTCTAGAGGCCGACTATAGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGACTATAGGC-4' (30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR-This library was enriched for
full-length clones and was constructed by Clontech
laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 737)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCACCGTCCGAGTCCCGACTCATGAGGAAGGATCATACCTATTTTGGGAATTTGCCACA 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACAGTTATGACATTGGGTTTGGGGTTTATTTTGAATGGACAGACTCTCCAAATGCTGCT 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            839 GAAAATTCCGAAAAAGTCCTTGAGCCAGAAGCTGCAGAAGAAGACCTTGGAAAATGGACCA 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        899 AAAGACTCTTCCAGTGATTGCAGCTCCATCCATGTGGACAAGACCACAAATCAAAGAC 958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: capbs_remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Horough the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI662 row: g column: 16
High quality sequence stop: 704.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 491.2; DB 12; Lewy....
Pred. No. 8.5e-106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:4808871"
/clone_lib="NIH_MGC_59"
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BG776473.1 GI:14046777
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87.38;
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a 140 c
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                                                                          human.
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AUTHORS
TITLE
JOURNAL
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                                                                                                                 /tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)."
/lab_host="DH10B (phage-resistant)."
/lote="Organ: prostate; Vector: pCWV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full:length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 CCAGACTGCCGTGCAGTTCCAGCTACTATGCAGCCCAACAGTATCCAGGGAACTACGAAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCTGGGGCATCATTGCCTGCATCATCAAGGTGAACACAGCTGGAGCAAGTGATACAC 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                        388 GGAGGAGCGAAGGCAGCGTGAAGAGGAAGAACGAGAGCGGCTGCAAAAGGAAGAAGA 447
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                                                                                                                                                                                                                                                                                                                                                          Query Match 34.3%; Score 499.8; DB 12; Best Local Similarity 84.8%; Pred. No. 7.9e-108; Matches 584; Conservative 0; Mismatches 102;
                                                                                                                                                                                                                                                                                       133 t
                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4475329"
                                                                                         /clone_lib="NIH_MGC_91"
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us-09-762-594-2.rst

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GGACAGGCCAAAACCCACACTGAAAATTCCGAAAAAGTCCTTGAGCCAGAAGCTGCAGAA 877
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BB704602.1 GI:16053437
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BB704602
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                                                                                                                                                                                                                                                                                                                                  EST 07-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Institutes of Health). Note: this is a NIH_MGC Library." 143 c 178 g 169 t
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 707)
1318
                                                                                                                 GTCTATCTCCTCAAGTTTGATAATTCCTACTCTGTGGAGGTCCAAGTCCGTCTACTAC 1378
                                                                                                                                                                        1379 AGAGTCTATTATACTAGATAGAGCTGCTGTTCCAAGGTCCGGAGTCCAGGGTTGAGCACA 1438
                                                                       NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Plate: LLAM10669 row: n column: 18
High quality sequence stop: 706.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 487.6; DB 12;
Pred. No. 6e-105;
); Mismatches 79;
                                                                                                                                                                                                                                                                                                                                  mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:4792145"
/clone_lib="NHH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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/db_xref="taxon:9606"
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87.3%;
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Best Local Similarity 87.3
Matches 557; Conservative
                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
BG705952
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BG705952
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BB704602 BERT II-OCT-2001 BB704602 RIKEN full-length enriched, in vitro fertilized eggs Mus musculus cDNA clone 7420465P14 3', mRNA sequence.
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatau, N., Hiramoto, K., Hiracka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawal, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinaki, T., Soqabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Kahiraki, T., Soqabe, Y., Suzuki, H., Tagawa, W., Tayanishi, A., Muramatsu, M. and Hayashizaki, Y. RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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The Institute of Physical and Chemical Research (RIKEN)
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GAAGCCTTGGAAAATGGACCAAAAGACTCTTCCAGTGATTGCAGCTCCATGTGG
                                                                                                                                                                                                                                                        ACAAGACCACAAAATCAAAGACTTTAAAGAGAAGATTCGGCAGGATGCAGATTCTGTGATT
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Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P. Shibata.Y., Hayatsu.N., Sugahara.Y., Shibata.K., Itoh
Carninci.P. Okazaki.Y. Hayatsu.N. and Hayashizaki.Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
perpare full-length cDNA libraries for rapid discovery of new
agi.K., Fujiwake.S., 10(10), 1617-1630 (2000)
wagi.K., Fujiwake.S., Inoue.K., Togawa,Y., Izawa,M., Ohara,E.,
Mattahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y. Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI" 102 c 125 g 107 t
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  Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                                                                                                                                                                                    'Y. and Hayashizaki,y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
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/clone_lib="RIKEN full-length enriched, in vitro
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/dev_stage="egg"
/lab_host="DH10B"
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99.2%; Pred. No. 1.8e-104;
iive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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1-7,-22 Suehiro-cho, T
Tel: 81-45-503-922
Fax: 81-45-503-9216
Email: genome-res@gsc
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/dev_stage="embryonic day 14.5 post-fertilization"
/note="Vector: paMP10 (Gibco); Cloned unidirectionally.
Primer: Oligo dT. RNA Isolation: Cytoplasmic RNA preps
(Manniatis); Cloning Technique: CUA Cloning (CloneAmp,
Life Technologies); Average insert size: 1.8 Kb;
Insertion site: TACGTCCACTGAATTCTGAGTG--->. Other
information regarding entire library may be found at
http://pga.swmed.edu/Data/Libraries/microarray_cdna_librar
ies.htm."
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4071-42 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
mRNA seguence.
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Mu.X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W., White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H. Gene expression in the developing mouse retina by EST sequencing
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/clone_lib="Mouse E14.5 retina lambda ZAP II Library"
/tissue_type="neural retina"
AATCAAAGACTTTAAAGAGAAGATTCGGCAGGATGCAGATTCTGTGATTACAGTACGTCG
                                                                                                                                                                                                                                                        1069 ATTTGCCACAGACAGTTATGACATTGGGTTTTGGGGTTTTTTGAATGGACAGACTCTCC
                                                       241 AATCAAAGACTTTAAAGAGAAAATTCGGCAGGATGCAGATTCTGTGATTACAGTACGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Biochemistry and Molecular Biology University of Texas M.D. Anderson Cancer Center Box 117, 1515 Holcombe Blvd., Houston, TX 77030, 17el: 713 792 3646 Fax: 713 790 0329.
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Nucleic Acids Res. 29 (24), 4983-4993 (2001)
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Pred. No. 1.3e-96;
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/organism="Mus musculus"
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Hammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

L (bases 1 to 625)

S Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt, J., Saed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.

Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray

L Unpublished (2000)

Contact: John Quackenbush

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 3528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gay, C., Holt
and
                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence
                                                                            GCGAGAGGAGGAAGACCGGC-TGAGACGGGAGGAGGAAGAGGCGGCGGCGGATAGAGGAAG 515
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                                           254
                                                                  TGATGTGTTGGGGAATGATAGGAGAGAGAATGGGCAGCTCTGGGAAACATGTCCAAGGA 276
                                                                                                             GGATGCCATGGTAGAGTTTGTGAAGCTTCTAAATAAGTGTTGTCCTCTCCTCTCGGCATA 336
                                                                                                                        GCGAAGGCAGCGTGAAGAAGGAAGAACGAGAGCGGCTGCAAAAGGAAGAAGAAGAAGCGGAA 456
                                                                                                                                                                                                                                                             AATAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGTTCGTGGCACT 194
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Pred. No. 1.5e-96;
0; Mismatches 93
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/clone_lib="MAGE resequences, ]
/ote="Vector: pBluescript5Km"
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84.8%;
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Plate: 192
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BE916087 649 bp mRNA linear EST 29-SEP-2000 601666710F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3966651 5',
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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CAGAGCAAACCCAACCTGCACAACAACAGGCAGCATTACAGAAACAGCAAGAAGTAGTGA 746
                                                                                                          TGGCTGGGGCATCATTGCCTGCATCAAGGTGAACACACAGCTGGAGCAAGTGATACAC 806
                                                                                                                                                                                                                                                                                                                                      AAGCTGCAGAAGAAGCCTTGGAAAATGGACCAAAAAGACTCTTCCAGTGATTGCAGCTC 926
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAMM140 row: c column: 04
High quality sequence start: 8
High quality sequence stop: 640.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1226 AACAAG-CCTCTGCTGGATGAGATT 1249
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Homo sapiens cDNA clone IMAGE:4340355 5',
                                                                              /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                           TGGCAGCTTTAAACTCGCAGA--CTGCCGTGCAATTCCAGC-AGTATGCAGCCCAGC-AG 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                          663
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                                                                                                                                                                   Length 649;
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                                                                                                                                                                                          Indels
                  /clone="IMAGE:3966651"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH108"
                                                                                                                                                                                          31;
                                                                                                                                                                   DB 12;
                                                                                                                                                                  tch 30.5%; Score 445.4; DB al Similarity 92.5%; Pred. No. 6e-95; 602; Conservative 0; Mismatches
           /db_xref="taxon:10090"
/strain="FVB/N"
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602257111F1 NIH_MGC_85
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Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 984)
                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Iymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Goran: lymph; Vector: pCWV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for full:length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                           Email: cgapDS-rémail.nih.gov
Tissue Procurement: Louis Staudt, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arraged by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9952 row: f column: 04
High quality sequence stop: 702.
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National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12; Length 984;
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Pred. No. 1.3e-91;
0; Mismatches 66;
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/clone="IMAGE:4340355"
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Best Local Similarity 87.8%;
Matches 482; Conservative (
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/db_xref='taxon:9606"
/db_xref='taxon:9606"
/dos_stage="Adult"
/dos_stage="Adult"
/note="Organ: Dreast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES POR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 519)

1 bolss Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PMl-BT0759-200 Seq primer: puc 18 forward High quality sequence start: 22 High quality sequence start: 22 High quality sequence store; 519.
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                                                                                                                            BE694778 11-SEP-2000 PMI-BE0759-200700-006-c03 BT0759 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 2.2e-85;
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BE694778.1 GI:10081938
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88.0%;
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Fax: +55-11-2707001
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/db_xref="taxon:10090"
/clone="lmAGE:5706182"
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/tissue_type="whole brain"
/tesue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
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/dev_stage="cont." brain: Vector: pYX-Asc; Site_1: EcoR I;
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/note="Organ: brain: Vector: phage resistant;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov acontact: Robert Strausberg, Ph.D. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
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This clone was contributed by the Brain Molecular Anatomy Project
1145 GTGCATGTCAGTGAGTCCAGTGACGAGGAGGAGGAGGAGGAAGAAAATGTCACTTGTGAA 1204
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                                                                                                                           GTTCGAGTACCCACCATGAAGAAGGATCATATCTTTTTTGGGAATTTGCCACAGACAAT 258
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           ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Ohin, Ph.D., program coordinator."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM804990 1114 bp mRNA linear EST 05-MAR-2002
AGENCOURT_6490228 NIH_MGC_125 Homo sapiens CDNA clone IMAGE:5725757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
cDNA was size selected according to mRNA size fraction,
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MIH MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                   AGTAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGTTCGTGGCACT 156
                                                                                                                                                                                                                                                                                                                                                                                                             TGATGTGTTGGGGAATGATAGGAGGAGAAATGGGCAGCTCTGGGAAACATGTCCAAGGA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                          GGATGCCATGCTAGAGTTTGTGAAGCTTCTAAATAAGTGTTGTCCTCTCCTCCGGCATA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGAAGGCAGCGTGAAGAGGAAGAACGAGAGGGCTGCAAAAGGAAAGAAGAAGCGGAA 456
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: Plate: LLAM12717 row: c column: 06
                                                                                                                                                                                                                                                                   GCATAAGCAAGTTCTTTTGGGCCCCATATAACCCAGACACGTCCCCTGAGGTTGGATTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCATAAGCAAGTTCTTTTGGGCCCATATAACCCAGACACGTCCCCTGAGGTTGGATTCTT
                                                                                                                                                                                                                                                                                                                                                                             TGATGTTGGGGAATGATAGGAGGAGAATGGGCAGCTCTGGGAAACATGTCCAAGGA
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                                                                                                                                                                                     Score 390.4; DB 14; Length 682; Pred. No. 6.4e-82; 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGAGAGGAGGACCGGCTGAGACGGGAGGA 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Emall: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 614.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM804990.1 GI:19121813
                                                                                                                                                                                      Query Match 26.8%;
Best Local Similarity 99.5%;
Matches 391; Conservative
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BM804990
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ORIGIN
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/db_xref="taxon:9606"
/clone="IMAGE:572575"
/clone="IMAGE:5725757"
/clone="IMAGE:5725757"
/clone="IMAGE:15"
/lab host="DH10B"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site_1: ECORV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gubber (Invitrogen). Research Genetics tracking code_33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456 AGCGAGAGGAGGAAGACCGGCTGAGACGGGAGGAGGAAGAGGGGGCGGCGGATAGAGGAAG 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 AGTAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGTTCGTGGCACT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCATAAGCAAGTTCTTTGGGCCCATATAACCCAGACACGTCCCCTGAGGTTGGATTCTT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGATGTGTTGGGGAATGATAGGAGGAGAGAATGGGCAGCTCTGGGAAACATGTCCAAGGA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCGAAGGCAGCGTGAAGAGGGAAGAACGAGAGCGGCTGCAAAAGGAAGAAGAGAGGAGGA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             516 AGAGGCTTCGGCTGGAACAGCAAAAGCAGATAATGGCAGCTTTAAACTCGCAGA--C 573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAGGCTTCCGGTGGAGCAGCAGAAAGCCGCAGATAATGGCAGCTTTAAACTCCCAGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        574 IGCCGIGCAATICCAGCAGIA-IGCAGCCCAGCAGI--AICCAGGGAACIACGAACAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTTGCGTCCCACAGAATAGAGAAGGAAGAAGAAGAGAAA-AAGAAGAAAGGCGGAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 368.6; DB 14; Length 1114; Pred. No. 9.5e-77;
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9
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                      /organism="Homo sapiens"
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84.5%;
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source
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//note="Organ: liver; Vector: PONR-LIB (Clontech); Site_1:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
sequence: S'-GGGGCATTATGGCC3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGCAGGGGCGCAATG-GT(30)BN-3' (where B = A,
c, of and N = A, c, G, or T). Average insert size 1:85
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NHL MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Upubblished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1533 row: h column: 01
High quality sequence stop: 627.
Location/Qualifiers
rce
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 639)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGAGACGGGAGGAGGAAGAAGAGGCGGCGGATAGAGGAAGAAGAGCTTCGGCTGGAACAG 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAAAGCAGCAGCAGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCCAGCAGTAT 595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 CAAAAGCAGCAGATAATGGCAGCTTTAAACTCCCAGACTGCCGTGCAGTTCCAGCATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGATTCTCATCCGCCAGCTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 25.2%; Score 367.4; DB 12; Length 639; al Similarity 84.1%; Pred. No. 1.8e-76; 497; Conservative 0; Mismatches 86; Indels 8;
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo saplens"
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/clone="IMAGE:4700208"
/clone=lib="NIH_MGC_76"
/lab_host="DH10B (TI phage-resistant)"
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                                                                  AUTHORS
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892 TGGACCAAAAGACTCTCCTTCCAGTGATTGCAGCTCCAT-CCATGTGGACAAGACCACA-A 949
                          482 GGACCACAAAGAATCTCTTCCAGTAATAGCAGCTCCATCCCATGTGGACACGACCTCAGA 541
                                                     Db
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Search completed: February 21, 2003, 23:27:09 Job time: 2239 secs

ATCAAAGACTT-TAAAGAGAAGATTCGGCAGGATGCAGATTCTGTGATTAC QΥ

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. No. No			•			SUMMARIES			
140.6 91.9 1543 10 AF022770 AF	Result No.	COL	* Query Match	Length		ID		scri	ion
779.6 74.0 2140 9 AK025520 AK005520 HR (000 4 61.0 3049 9 DE004552 D HR (000 4 61.0 3049 9 DE004552 D HR (000 4 61.0 3049 9 DE004553 D HR (000 4 61.0 3049 9 DE004553 D HR (000 5 6 597) 1 18440 10 DE004553 D HR (000 5 2 MC) 1840 10 AC012029 AC014825 D AC		340	91.9	1543	10	AF02277		AF02277	Mus m
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Li.H. and Papadopoulos, V.
Direct Submission
Submitted (12-APR-2000) Department of Cell Biology, Georgetown University Medical Center, 3900 Reservoir Rd. NW, Washington,
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Li,H. and Papadopoulos,V.
Direct Submission
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                               Mol. Endocrinol. 15 (12), 2211-2228 (2001) 21588728
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Direct Submitsed (29-806-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dal, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
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EERLRREEEERRRIEGOGKOJIMAALNSOTAVOFQOYAAOOYFGOTA
IRQLOEOHYQQYWQQLYQVQLAQQQAALQKQOEVVVAGSSLPTSSKVNATVPSNMMSV
NGQAKTHTDSSEKELEPEAAEEALENGPRESILPVIAAPSMWTRPQIKDFKEKIQQDAD
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SDDDEEEEENIGCEEKAKKNANKPLLDEIVPVYRRDCHEEVYAGSHQYPGRGVYLLKF
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                                                             clone_lib:HEP
                                                                                                       Euteleostomi;
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                                            oligo capping; fis (full insert sequence).
Homo sapiens hepatoma cell_line:HepG2 cDNA
clone:HEPO2419.
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/cell_type="hepatoma"
/clone_lib="HEP"
/note="cloning vector pME18SFL3"
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/db_xref="G1:10438061"
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/protein_id="BAB2059.2"
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HPTYEEKLKLVALHKQVLMGPYNPDTCPEVGFFDVLGNDRRREWAALGNMSKEDAMVE
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EERLAREEEERRRIEEERLALBOOKOOIMAALNSQTAVOFOOYAAQOYPGNYEQOIL
IRQUEGHYROOYMOOLYOOLAQOAALOKOOFVAGSSLETSEKVARTPESNMSY
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SDDDEEEEENIGCEEKAKKNANKPLLDEIVPVYRRDCHEEVYAGSHQYPGRGVYLKK
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Homo sapiens gcp60 mRNA for golgi resident protein GCP60, complete
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On Sep 27, 2001 this sequence version replaced gi:12060408.
                                                                                                                                                                                                                                                                                               Identification and characterization of a novel Golgi protein, GCP60, that interacts with the integral membrane protein giantin 1576.78
AGTAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGTTCGTGGCACT 156
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Ikehara,Y.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HeCa"
/note="vector:HB814"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (24-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 21 Row: c Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.
Richards, S., Gibbs, R.A.
                                                                                                                   1416
complex associated protein
                  GCGGTCAAAATCAGTCTACTACAGAGTCTATTATACTAGATAAAAATGTTGTTACAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
                                                        CCACCAGTATCCAGGGGGGGGGGTCTATCTCCTCAAGTTTGATAATTCCTACTCTCTGTG
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Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
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/clone_lib="NHI_MGC_66"
/lab_host="DH108"
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                                                                                                                                                                          /note="Vector: pCMV-SPORT6"
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Contact: MGC help desk
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PGNYEQQQILIRQLOBQHYQQYMQQLYQVQLAQQQAALQKQQEYVVAGSSLEPTSSKVN
YPVSNMMSVNGQAKTHTDSSEKELEPBAAEERLENGFKESLEVIAAPSMWTRQJKD
FKEKIQQDADSVITYRGREVYTVRVPTHEEGSYLFWEFATDNYDIGFGVYFFWTDSPN
TAVSVHVSESSDDDEEEEENIGCEEKAKKNANKPLLDEIVPVYRRDCHEEVYAGSHQY
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GLGSGASGQQREPGEAAAEGAAEEARRMEQHWGFGLEELYGLALRFYKIKDGRAFHPT
SEEKLKFVALHKQVLLGPYNDTSPEVGFFDVLGADRRRAMALGMWSREDAWTFVK
LLNKCCPLLSAYVASHIRIEREERRRAFEERRRANGREEERRRAKEEBEDR
LRREEEFRRIEEFRRIEEFRRALEGOKQQIMAALNSOTAVQFQQYAAQQYPGNYEQQQILIRQ
LQDGHYQQYMQQLYQVVQLAQQQAALOKQQFWAAGASLPASSKVWTAGASDTLSVNG
AKTHTENSERVLEPFRAAEALBWGFNSLPVIAAPSWWTRQQINGFKRIRQDBSVI
TYRREEWYTYRYPPIHEGSSYLEWBFRYDSYDIGFGYYFEWTDSPUAANSVHYSESSBE
EEEEEEWVTYRYPPIHEGSSYLEWBFRYDSYDIGFGYYFEWTDSPUAANSVHYSESSBE
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Liu,J. and Papadpoulos,V.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"peripherial benzodiazepine receptor associated protein PAP7"
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.15330,16955. .17228)
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10857. .11031,13325. .13511,15046.
/gene="Pap7"
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/gene="Pap7"
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/db_xref="GI:20453989"
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/organism="Mus musculus"
/strain="BALB/c"
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Streen, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Burren, B., Linton, L., Nusbaum, C., Campopiano, A., Chang, J., Chazaro, B., Cooepel, Y., Colamarata, J., Campopiano, A., Chang, J., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzlaph, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Karatas, A., Kells, C., Lancocque, K., Landzares, R., Landers, T., Lehoczky, J., Marquis, N., Matthews, C., Macchan, P., McKarnan, K., Maldrim, J., Mathews, C., McCarthy, M., McEban, P., McKornan, K., Moldrim, J., Mathews, C., McCarthy, M., McEban, P., McKornan, K., Moldrim, J., Mathews, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nonnell, P., O'Nonnell, P., O'Nonnell, P., O'Nonnell, P., O'Nonnell, P., O'Norman, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Schauer, S., Schupback, R., Schauer, S., Schupback, R., Stantos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Volal, R., Vola, Milson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Charlett, M., Man, D., Ye, W.J., Young, G., Subrission, L., Zimmer, A. and Zody, M.
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LOW-PASS SEQUENCE SAMPLING.
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Center: Whitehead Institute/ MIT Center for Genome Research
ACAGACAGTTATGACATTGGGGTTTATTTTGAATGGACAGACTCTCCAAATGCT
                                                                                                                                                 1016 GTCGTCACCGTCCGAGTCCCGACTCATGAGGAAGGATCATACCTATTTTGGGAATTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15279 GCTGTCAGTGTGCATGTCAGTGAGTCCAGTGACGAGGAGGAGGAGGAGGAG 15330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mus musculus clone RP23-172B15,
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* NOTE: This record contains 79 individual

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sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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21812: contig of
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22605: contig of
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25037: contig of
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1503: contig of
1603: gap of 10
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                                                                                                                                                        1;
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Eukaryota.

Butharia: Chordata, Craniata; Vertebrata; Euteleostomi;

Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 140409)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 1, clone RP11-275114
                                                                                                                                                                                                                                                 33842 AGTCCGTCTACTACAGAGTCTATTATACTAGATAGAGCTGCTGTTCCAGGGTCGGGAGTC 33901
                                                                                                                                                                                                              1186 AGAAAATGTCACTTGTGAAGAAAAAAGAAGAACGCCAACAACAAGACTCTGCTGGATGA 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCCAGGGAGGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTCTGTGGAGGTCCA 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTCCGTCTACTACAGAGTCTATTATACTAGATAGAGCTGCTGTTCCAAGGTCCGGAGTC 1424
                                                                                                                                                                                                                                                                                                                                       GATTGTACCTGTGTACCGGC-GGGACTGTCACGAGGAAGTATATGCAGGCAGCCACCAGT 1304
                                                                                                                                                        Gaps
                                                                                                                                                     1;
                                                                                        Length 63971;
                                                                                                                                                     Indels
55160 55872: contig of 713 bp in length
55873 55972: gap of 100 bp
                                                                                            DB 2;
                                                                                        Score 246.2; DB 2
Pred. No. 1.3e-51;
                                                                                                                                                     0; Mismatches
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AC044825.2 GI:9502452
HTG; HTGS_PHASE1; HTGS_DRAFT.
HOmo sapiens.
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REFERENCE
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------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                         vector: M13; M77815; 99% of reads
vector: Plasmid; n/a; %-0.f%% of reads
                                                                                                                Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus quality: 120391 bases at least Q40 Consensus quality: 129577 bases at least Q30 Consensus quality: 133768 bases at least Q20 Insert size: 160000; agarose-fp Insert size: 136609; sum-of-contigs Quality coverage: 3.1 in Q20 bases; agarose-fp Quality co.
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of 1128 bp in length
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of 1009 bp in length
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15578: gap of 100 bp
1753: contig of 2175 bp in length
17553: gap of 100 bp
19331: contig of 1478 bp in length
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25903: contig of 2667 bp in length
26003: gap of 100 bp
29651: contig of 3648 bp in length
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41171 43345: contig of 2175 bp in length
43346 4345: gap of 100 bp
43346 46364: contig of 2919 bp in length
46365 46464: gap of 100 bp
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of 1714 bp in length
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35597: contig of 2496 bp in length
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contig of 1854 bp
                                                                                                                                                                                                                                            2266 2365; gap of 2366 23576; contig of 12 23676; gap of 100 3577 3676; gap of 100 4846 4945; gap of 24 7367; contig of 24 7367; gap of 100 7468 8695; gap of 100 8596 8695; gap of 100 8596 8695; gap of 100 8696 10409; contig of 11 8596 8695; gap of 100 8696 10409; contig of 11 100 8696 10409; contig of 11 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 100 8696 10
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1257 2265: contig of
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33001: con+
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23136: cont
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us-09-762-594-2.rge

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89531 89630: contig of 5317 bp in length 89531 89630: gap of 100 bp 89531 89649: contig of 5317 bp in length 94948 95047: gap of 100 bp 9548 100827: contig of 5317 bp in length 10828 100927: gap of 100 bp 10590: gap of 100 bp 105901 105900: gap of 100 bp 105901 114896: contig of 8996 bp in length 114897 114996: gap of 100 bp 114997 12717: contig of 12121 bp in length 12718 127217: gap of 100 bp 127218 127217: gap of 100 bp 127218 127217: gap of 13192 bp in length.
                                                                                                                                                                                                      49423: gap of 100 bp
52514: contig of 3091 bp in length
52614: gap of 100 bp
56594: contig of 3980 bp in length
                                                                      100 bp
3646 bp in length
                                                                                                     p of 100 bp
contig of 4053 bp in length
                                                                                                                                contig of 4052 bp in length
                                                                                                                                                                                         71601: gap of 100 bp 74120: contig of 2519 bp in length
                                                                                                                                                                                                                                                                                  89530: contig of 5696 bp in length
                                                                                                                                                               100 bp 7 2756 bp in length
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note="assembly_fragment"
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'note="assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
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note≂"assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
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/db_xref="taxon:9606"
                                                                    56694: gap of 1
60340: contig of
49323: contig of
                                                                                                                                                                             contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="RP11-275114"
                                                                                                                                                  cont
-3: gap of
71501:
                                                                                                60440: gap of
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              49324
49424
52515
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56695
60341
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64494
64594
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HTG 17-AUG-2002
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1 (bases 1 to 181719)
11 (bases 1 to 181719)
12 (bases 1 to 181719)
13 (bases 1 to 181719)
14 (bases 1 to 181719)
15 (bases 1 to 181719)
16 (bases 1 to 181719)
17 (bases 1 to 181719)
18 (bases 1 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTGTCAGTGTGCATGTCAGTGAGTCCAGTGACGAGGAGGAGGAGGAAGAAAATGTC 1195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           896 CCAAAAGACTCTTCCAGTGATTGCAGCTCCATCCATGTGGACAAGACCACAAATCAAA 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAGACAGTTATGACATTGGGGTTTGGGGTTTATTTTGAATGGACAGACTCTCCAAATGCT
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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Sequencing vector: M13; M77815; 0% of reads
Sequencing vector: plasmid; L08752; 99% of reads
Chemistry: Dye-primer-amersham; 0% of reads
Chemistry: Dye-terminator; 9% of reads
                                                                                                                                                                                                                                                                                                                                                                                Score 238; DB 2; I
Pred. No. 1.7e-49;
0; Mismatches 50;
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/note="assembly_fragment"

38065. 41070

/note="assembly_fragment"

41171. 43345

/note="assembly_fragment"

43446. 46364
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                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.3%;
Best Local Similarity 84.3%;
Matches 268; Conservative
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AL592045/c
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19473:
    HTG; HTGS_PHASE1.
                                         Homo sapiens
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2447
22447
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10910
112204
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                                         ORGANISM
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JOURNAL
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AUTHORS
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AUTHORS
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  KEYWORDS
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DD 105039 GACTTCAAAGAAGAATCAGCAGGATGCAGATTCCGTGATTACAGTGGGCCCGAGGAAA 104980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DD 104979 GTGGTCACTGTTCGAGTACCCACCCATGAAGGATCATATCTCTTTTGGGAATTTGCC 104920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 104919 ACAGACAATTATGACATTGGGGTGTATTTTGAATGGACAGACTCTCCCAAACAT 104860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 104859 GCTGTCAGCGTGCATGTCAGCGATGACGACGAGGAGGAGGAAGAAGAAGGTAGACC 104800
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              Dye-terminator Big Dye; 90% of reads
Consensus quality: 181214 bases at least Q40
Consensus quality: 18143 bases at least Q30
Consensus quality: 181535 bases at least Q20
Insert size: 181619; sum-of-contigs
Insert size: 184421; 3.1% error; agarose-fp
Quality coverage: 12.97x in Q20 bases; sum-of-contigs Quality
coverage: 13.26x in Q20 bases; agarose-fp
Chemistry: Dye-terminator ET-amersham; 0% of reads Chemistry:
                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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Pred. No. 1.7e-49;
0; Mismatches 50;
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42290 c 42015 g 47265 t
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clone_end:SP6
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/db_xref="taxon:9606"
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Direct Submission (21-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 40 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                        MO 63108, USA
On Aug 25, 2000 this sequence version replaced gi:9838290
                                                                                                                                                                                                                                                                                                          Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemistry: Dye-primer ET; 86% of reads Chemistry: Dye-terminator Blg Dye; 14% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 211766 bases at least Q40 Consensus quality: 217990 bases at least Q30 Consensus quality: 221643 bases at least Q20 Insert size: 181000; agarose-fp Insert size: 228280; sum-of-contigs Quality coverage: 6.35 in Q20 bases; sum-of-contigs Quality coverage: 4.69 in Q20 bases; sum-of-contigs
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Sequencing vector: plasmid; 14%
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165082: contig of 30962 bp in length 165182: gap of unknown length 196240: contig of 31058 bp in length 196340: gap of unknown length 196340: gap of unknown length 196340: gap of area.
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/note="assembly_name:Contig15"
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Db 178869 GACTTCAAAGAAGAAGATTCAGCAGGATGCAGATTCCGTGATTACAGTGGGCCCGAGGAA 178810

        QY
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        GCTGTCAGTGGCATGTCAGTGAGTCCAGTGAGGAGGAGGAGGAGGAAGAAATGTC
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/note="assembly_name:Contig69"
42675. .44938
/note="assembly_name:Contig70"
45039. .50126
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/note="assembly_name:Contig71"
50227. .52594
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52695. .57156
/note="assembly_name:Contig73"
                                                                                                                                                                                                                                                                   22500. .24200
/note="assembly_name:Contig59"
24301. .25667
/note="assembly_name:Contig60"
25768. .27705
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27806. .29643
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29744. .31718
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Llarity 84.3%; Pred. No. 1.8e-49;
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                                                                               /note="assembly_name:Contig53"
15083. .16905
/note="assembly_name:Contig54"
                                                                                                                               17006. .18051
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18152. .19373
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13643. .14982
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Muzny, D.M., Adams, C., Adlo-Oddola, B., All-osman, F.R., Allen, C., Ats. Alstrooks, S. L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Battaria, J., Benton, J., Blimage, H.C., Are, J.R., Ayele, M., Banks, T., Battaria, J., Benton, J., Blimage, H.C., Are, J.R., Ayele, M., Brant, D., Butaria, J., Benton, J., Blimage, H.C., Blower, J., Brown, M., Bryant, N.P., Butaria, J., Butkett, C., Burch, P., Burkett, C., Burch, J., Chavez, D., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Clen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Clen, R., Coyle, M.D., Ding, Y. Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Douthwaite, K.J., Brand, C.D., Carcal, H., Dugan-Rocha, S., Durbin, K.J., Falls, T., Garz, J., Garza, N., Gill, R., Gabisli, H., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gabisli, H., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Harris, C., Harris, K., Habrik, P., Hawes, A., Hernandez, J., Howard, S., Hober, J., Haylak, P., Hawes, A., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Harris, C., Harris, K., Hatt, M., Jollycet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvar, J., Kovar, C., Kratvovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L. Li, J., Lichtarge, O., Lieu, C., Liu, J., Liu, R., Martin, M., Mansew, M., Noiresson, J., Nowtson, J., Nowtson, J., Nowtson, J., Markes, M., Ren, Y., Riwes, M., Rojas, A., Rojas, A., Paycon, B., Paycon, B., Baych, M., Sarales, M., Rojas, A., Rojas, A., Paycon, B., Paycon, B., Baych, R., Sonch, R., Sarete, S., Warten, R., Sonch, R., Walliamson, K., Wayelliamson, S., Warten, R., Washington, C., Way, Y., Wu, Y. F., Pulliamson, A., Willelland, S., Warten, R., Sanker, S., Warten, R., Washington, S., Walliams, G., Williams, G., Walliams, S., Warten, R., Walliams, 
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Rattus norvegicus clone CH230-162N10, *** SEQUENCING IN PROGRESS
***, 70 unordered pieces.
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Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
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                                                                                                                                                                                                                                                                                                                                                                                                                Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                               AC126290.2 GI:21702826
HTG; HTGS_PHASE1.
                                               Db 178629 CTTGGTCCATATTCAGTA 178612
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Direct Submission
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Baylor Plaza, Houston, TX 77030, USA
On Jul 7, 2002 this sequence version replaced gi:21699099.
                                                                                                                                                                                               Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
                                                                                                                                                                                                                               Assembly program: Phrap, version 0.990329
Consensus quality: 107819 bases at least Q40
Consensus quality: 114791 bases at least Q30
Consensus quality: 119520 bases at least Q20
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                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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PRI 01-AUG-2002

Euteleostomi;

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Rawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R.,
Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J.,
Isono, Y., Kawai-Hio, Y., Salto, K., Nishikawa, T., Kimura, K.,
Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H.,
Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K.,
Takahashi, Puji, A., Oshima, A., Suzuki, Y., Sugano, S., Nagahari, K.,
Masuho, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
 1306 TCCAGGGAGGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTGTGTGGAGGTCCAA
                                             GTCCGTCTACTACAGAGTCTATTATACTAGATAGAGCTGCTGTTCCAAGGTCCGGAGTCC
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                  2235 bp mRNA linear
Homo sapiens cDNA FLJ32556 fis, clone SPLEN1000134.
AK057118
                                                                                                                                                                                                                                                                                                                   oligo capping; fis (full insert sequence).
Homo sapiens spleen cDNA to mRNA, clone_lib:SPLEN1
clone:SPLEN1000134.
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Submitted (24-007-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics&hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan KRY Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and
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Pred. No. 7.2e-43;
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Isogai,T., Otsuki,T. and Sugiyama,T.
Direct Submission
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/db_xref="taxon:9606"
/clone="splent1000134"
/tissue_type="spleen"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1306 TCCAGGGAGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTCTGTGGAGGTCCAA 1365
                1656 TCCAGGGAGAGGAGTCTATCTCCTCAAGTTTGACAACTCCTACTCTTTGTGGCGGTCAAA 1715
                                                        GTCCGTCTACTACAGAGTCTATTATACTAGATAGAGCTGCTGTTCCAAGGTCCGGAGTCC 1425
                                                                        1337 GATAATTCCTACTCTGTGGAGGTCCAAGTCCGTCTACTACAGAGTCTATTATACTAGA 1396
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AK095650 3547 bp mRNA linear PRI 15-JUL-2002 Homo sapiens CDNA FLJ3831 fis, clone FCBBF3025285, moderately similar to Mus musculus peripherial benzodiazepine receptor
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NOTE: This is a 'working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as Thus of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamtari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) Who EDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA full insert sequencing: Construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- 6 3'-end one pass sequencing: RAB, HIX, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M.,
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Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K.,
Masuho, Y., Nagai, K. and Isogai, T.
                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                              oligo capping; fis (full insert sequence).
Homo sapiens fetal brain cDNA to mRNA, clone_lib:FCBBF3
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/note="cloning vector
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Isogai, T. and Yamamoto, J.
Direct Submission
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Patent: WO 0218424-A 238 07-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1232 CCTCTGCTGGATGAGATTGTACCTGTGTACCGGGGGACTGTCACGAGGAAGTATATGCA 1291
                                                                                                                  GGCAGCCACCAGTATCCAGGGAGGGGAGTCTATCTCTCCTCAAGTTTGATAATTCCTACTCT 1351
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1.882
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